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(54) Title: SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

(57) Abstract

Secreted expressed sequence tags (sESTs) isolated from a variety of human tissue sources are provided.

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SECRETED EXPRESSED SEQUENCE TAGS (sESTs)

5

FIELD OF THE INVENTION

The present invention provides novel polynucleotides which are expressed sequence tags (ESTs) for secreted proteins.

BACKGROUND OF THE INVENTION

10 Gargantuan efforts have been employed by various investigational projects to randomly sequence portions of naturally-occurring cDNAs. The rationale behind this approach to identification and sequencing genes is founded in two basic principles: (1) that transcribed cDNAs represent the product of the most important genes, namely those that are actually expressed *in vivo*, and (2) that efforts to sequence genes and other portions of the genome of
15 target organisms which are not actually expressed wastes substantial effort on areas not likely to yield genetic information of therapeutic importance. Thus, the high-throughput sequencing efforts focus on only those portions of the genome which are expressed. The randomly produced cDNA sequences represent "expressed sequence tags" or "ESTs", which identify and can be used as probes for the longer, full-length cDNA or genomic sequence from which they
20 were transcribed.

Although this "shortcut" approach to genomic sequencing presents savings of effort compared to sequencing of the complete genome, it still produced a vast array of ESTs which may not be directly useful as protein therapeutics. To date, the majority of protein-related drug discovery has focused on the use of secreted proteins to produce a desired therapeutic effect.

25 Since the EST approach theoretically identifies all expressed proteins, it produces an EST library which contains a mixture of secreted proteins (such as hormones, cytokines and receptors) and non-secreted proteins (such as, for example, metabolic enzymes and cellular structural proteins), without identifying which ESTs correspond to proteins falling into either category. As a result, these methods are not optimally tailored to the needs of investigators
30 searching for secreted proteins because they must separate the secreted "wheat" from the non-secreted "chaff", wasting effort and resources in the process.

35 Co-assigned U.S. Patent No. 5,536,637, which is incorporated herein by reference, provides methods for focusing genomic sequencing efforts on sequences encoding the secreted proteins which are of most interest for identification of protein therapeutics. The '637 patent discloses a "signal sequence trap" which selectively identifies ESTs for secreted

proteins, namely "secreted expressed sequence tags" or "sESTs". It is to these sESTs that the present invention is directed.

SUMMARY OF THE INVENTION

5 The present invention provides for sESTs isolated from a variety of human RNA/cDNA sources.

In preferred embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ
10 ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID
NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ
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ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ
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or a complement of said sequence.

15 In other embodiments, the present invention provides an isolated polynucleotide consisting of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ

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2 ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100.
3 SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID
4 NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
5 SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
6 NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118,
7 SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID
8 NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
9 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
10 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
11 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
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13 SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
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16 NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
17 SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
18 NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
19 SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
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21 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
22 NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190,
23 SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
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31 SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
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or a complement of said sequence.

In further embodiments, the present invention provides an isolated polynucleotide consisting essentially of a nucleotide sequence selected from the group consisting of:

SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ

15 ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, SEQ ID NO:121, SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

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30 or a complement of said sequence.

In yet other embodiments, the present invention provides an isolated polynucleotide comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of:

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5 or to a complement of said sequence.

The invention also provides for proteins encoded by the above-described polynucleotides.

10

DETAILED DESCRIPTION

The nucleotide sequences of the sESTs of the present invention are reported in the Sequence Listing below. Table 2 lists the "Clone ID Nos." assigned by applicants to each SEQ ID NO: in the Sequence Listing.

15 Table 2

Each pair of entries in this table consists of the SEQ ID NO (e.g., 1, 2, etc.) followed by the Clone ID No. for such sequence (e.g., B11, B18, etc.).

1	BV31	18	CB302	35	BZ83	52	CD244	
2	BV34	19	CB318	36	BZ87	53	CD265	
20	3	BV37	20	CB321	37	CB15	54	BT217
4	BV45	21	CB96	38	CB2	55	BV278	
5	BV8	22	CB98	39	CB44	56	BV280	
6	BV93	23	BZ42	40	CC11	57	BV282	
7	BV99	24	BZ53	41	CC182	58	BV285	
25	8	CB100	25	BZ56	42	CC298	59	BV286
9	CB107	26	BZ6	43	CC310	60	BV291	
10	CB110	27	BZ607	44	CC323	61	BV295	
11	CB114	28	BZ61	45	CC332	62	BW389	
12	CB118	29	BZ62	46	CC335	63	BX135	
30	13	CB123	30	BZ641	47	CC338	64	BX141
14	CB129	31	BZ644	48	CC41	65	BX148	
15	CB137	32	BZ72	49	CC52	66	BZ1	
16	CB239	33	BZ74	50	CD107	67	BZ16	
17	CB259	34	BZ82	51	CD205	68	BZ187	

69	BZ19	103	CE159	137	CH315	171	CC194	
70	BZ205	104	CE2	138	CH325	172	CC198	
71	BZ222	105	CE347	139	BZ568	173	CC199	
72	BZ230	106	CE36	140	BZ578	174	CC205	
5	73	BZ234	107	CE40	141	BZ588	175	CC215
	74	BZ244	108	CE87	142	BZ597	176	CC253
	75	BZ269	109	CG1	143	BZ598	177	CC258
	76	BZ280	110	CG44	144	CH637	178	CC259
	77	BZ288	111	CG60	145	CH644	179	CC265
10	78	BZ304	112	CG68	146	CH699	180	CC288
	79	BZ328	113	BP202	147	CI240	181	CC95
	80	BZ331	114	BP242	148	CI247	182	CC96
	81	BP646	115	BP243	149	CJ1	183	CD311
	82	BP652	116	BZ444	150	CJ19	184	CD323
15	83	BP656	117	BZ453	151	CJ24	185	CH338
	84	BP666	118	CC233	152	CJ27	186	CH355
	85	BP667	119	CC242	153	CJ3	187	CH377
	86	BP674	120	CC247	154	CJ37	188	CH421
	87	BP695	121	CC344	155	CJ42	189	CH425
20	88	BP705	122	CC346	156	CJ44	190	CH522
	89	BP713	123	CC351	157	CJ49	191	CH541
	90	BP720	124	CC359	158	CJ50	192	CH555
	91	BP750	125	CC364	159	CJ55	193	CH558
	92	BP754	126	CC365	160	CJ6	194	CH582
25	93	BW143	127	CC374	161	CJ76	195	CH595
	94	BR307	128	CE303	162	CJ77	196	CH720
	95	BR309	129	CE328	163	CJ84	197	CH723
	96	BR312	130	CG199	164	CJ86	198	CH724
	97	BR318	131	CG209	165	CJ91	199	CH735
30	98	CB187	132	CG210	166	CC111	200	CH742
	99	CB190	133	CG350	167	CC118	201	CI126
	100	CB204	134	CG354	168	CC120	202	CI129
	101	CB213	135	CG426	169	CC126	203	CI133
	102	CE120	136	CH303	170	CC130	204	CI181

	205	CI229	239	CG160	273	CI395	307	CJ397
	206	CI25	240	CG175	274	CI407	308	CJ400
	207	CI52	241	CG176	275	CI411	309	CJ404
	208	CI84	242	CG180	276	CI437	310	CJ415
5	209	CI91	243	CG279	277	CI443	311	CJ420
	210	BP163	244	CG292	278	CI444	312	CJ424
	211	BP175	245	CG300	279	CI459	313	CJ434
	212	BP199	246	CG301	280	CI480	314	CJ454
	213	BP272	247	CG314	281	CI490	315	CJ457
10	214	BP284	248	CG315	282	CI492	316	CJ481
	215	BP294	249	CG324	283	CI493	317	CJ493
	216	BP299	250	CG336	284	CI510	318	CJ501
	217	BP300	251	CG99	285	CI522	319	CJ514
	218	BP306	252	CH143	286	CI534	320	CJ539
15	219	BP311	253	CH207	287	CI542	321	CJ540
	220	BP312	254	CH224	288	CI560	322	CJ549
	221	BP327	255	CH227	289	CI561	323	CJ551
	222	BP345	256	CH245	290	CI583	324	CK126
	223	BP368	257	CH246	291	CI586	325	CK151
20	224	BP467	258	CH27	292	CJ145	326	CK181
	225	BP468	259	CH30	293	CJ149	327	CK201
	226	BR375	260	CH4	294	CJ160	328	CK213
	227	BR390	261	CH64	295	CJ164	329	CK218
	228	BR408	262	CH78	296	CJ168	330	CK234
25	229	BR418	263	CH85	297	CJ176	331	CK37
	230	BY66	264	CH87	298	CJ183	332	CK48
	231	CF118	265	CN320	299	CJ194	333	CL104
	232	CF127	266	CN343	300	CJ206	334	CL110
	233	CF22	267	CN344	301	CJ230	335	CL122
30	234	CF235	268	CN395	302	CJ237	336	CL132
	235	CG109	269	CN423	303	CJ257	337	CL147
	236	CG131	270	CI363	304	CJ265	338	CL152
	237	CG153	271	CI386	305	CJ378	339	CL181
	238	CG158	272	CI392	306	CJ389	340	CL182

	341	CL399	375	CN516	409	CO58	443	CO155
	342	CL469	376	CN532	410	CO48	444	CO153
	343	CL470	377	CN552	411	CO444	445	CO145
	344	CL481	378	CN593	412	CO431	446	CO140
5	345	CL493	379	CN619	413	CO391	447	CO139
	346	CM12	380	CN621	414	CO384	448	CO128
	347	CM178	381	CN667	415	CO36	449	CO1254
	348	CM188	382	CN703	416	CO351	450	CO1247
	349	CM194	383	CN718	417	CO337	451	CO1232
10	350	CM246	384	CN729	418	CO327	452	CO1224
	351	CM251	385	CN835	419	CO315	453	CO1223
	352	CM54	386	CN896	420	CO304	454	CO1206
	353	CM62	387	CO933	421	CO270	455	CO1198
	354	CN140	388	CO924	422	CO268	456	CO1196
15	355	CN171	389	CO908	423	CO264	457	CO1194
	356	CN173	390	CO900	424	CO261	458	CO1187
	357	CN238	391	CO889	425	CO257	459	CO1180
	358	CN29	392	CO888	426	CO253	460	CO1178
	359	CN291	393	CO874	427	CO25	461	CO1175
20	360	CN304	394	CO851	428	CO246	462	CO117
	361	CN327	395	CO83	429	CO244	463	CO1168
	362	CN49	396	CO821	430	CO240	464	CO1164
	363	CN50	397	CO806	431	CO228	465	CO1162
	364	CN54	398	CO798	432	CO223	466	CO1161
25	365	CN65	399	CO79	433	CO222	467	CO1159
	366	CJ305	400	CO71	434	CO209	468	CO1153
	367	CJ316	401	CO7	435	CO205	469	CO1151
	368	CJ317	402	CO69	436	CO204	470	CO1137
	369	CJ336	403	CO66	437	CO20	471	CO1123
30	370	CJ347	404	CO639	438	CO197	472	CO1076
	371	CJ360	405	CO638	439	CO185	473	CO1072
	372	CJ365	406	CO625	440	CO170	474	CO1026
	373	CJ366	407	CO62	441	CO17	475	CO1000
	374	CN483	408	CO602	442	CO163	476	CN755

	477	CN736	511	CR1166	545	CR632	579	CO409
	478	CN709	512	CR1186	546	CR641	580	CO474
	479	CO975	513	CR1190	547	CT729	581	CO480
	480	CO990	514	CR329	548	CN922	582	CO500
5	481	CP280	515	CR354	549	CN934	583	CO519
	482	CP283	516	CR377	550	CN951	584	CO522
	483	CP287	517	CR390	551	CN952	585	CO526
	484	CP289	518	CR392	552	CN980	586	CO559
	485	CP294	519	CR422	553	CP111	587	CO595
10	486	CP304	520	CR423	554	CP147	588	CO605
	487	CP307	521	CR466	555	CU13	589	CO618
	488	CP311	522	CR477	556	CP251	590	CO629
	489	CP313	523	CR478	557	CP258	591	CO643
	490	CP314	524	CR482	558	CP33	592	CO653
15	491	CP328	525	CR491	559	CP41	593	CO661
	492	CP352	526	CR494	560	CP91	594	CO667
	493	CQ286	527	CR502	561	CP92	595	CO695
	494	CQ294	528	CR506	562	CQ160	596	CO696
	495	CQ304	529	CR513	563	CQ165	597	CO707
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	497	CQ331	531	CR515	565	CQ30	599	CO718
	498	CQ333	532	CR527	566	CR100	600	CO720
	499	CR1116	533	CR529	567	CR178	601	CO722
	500	CR1118	534	CR537	568	CR184	602	CO736
25	501	CR1121	535	CR538	569	CR263	603	CO763
	502	CR1127	536	CR540	570	CR335	604	CO767
	503	CR1135	537	CR541	571	CR4	605	CP116
	504	CR1141	538	CR545	572	CR61	606	CP151
	505	CR1142	539	CR587	573	CR93	607	CI293
30	506	CR1144	540	CR588	574	CO282	608	CI294
	507	CR1147	541	CR593	575	CO310	609	CI298
	508	CR1155	542	CR594	576	CO334	610	CU14
	509	CR1156	543	CR611	577	CO387	611	CU2
	510	CR1162	544	CR618	578	CO390	612	CU25

	613	CU32	647	CR678	681	CT748	715	CS520
	614	CU39	648	CR726	682	CT738	716	CS524
	615	CU40	649	CR733	683	CT726	717	CS534
	616	DA10	650	CR778	684	CT706	718	CT14
5	617	DA136	651	CR836	685	CT705	719	CT142
	618	DA155	652	CR839	686	CT702	720	CT143
	619	DA16	653	CR872	687	CT693	721	CT149
	620	DA165	654	CR890	688	CT677	722	CT156
	621	DA170	655	CR916	689	CT658	723	CT159
10	622	DA183	656	CR929	690	CT645	724	CT162
	623	DA223	657	CR930	691	CT636	725	CT188
	624	DA224	658	CR936	692	CT631	726	CT189
	625	DA225	659	CR974	693	CT616	727	CT190
	626	DA227	660	CT747	694	CT611	728	CT193
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	633	DA490	667	CT864	701	CS271	735	CT227
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	639	DA516	673	CT797	707	CS319	741	CT275
	640	DA529	674	CT791	708	CS322	742	CT28
	641	DA84	675	CT785	709	CS353	743	CT284
30	642	CR1003	676	CT783	710	CS366	744	CT293
	643	CR1013	677	CT780	711	CS471	745	CO1020
	644	CR1044	678	CT771	712	CS475	746	CO1043
	645	CR1056	679	CT754	713	CS485	747	CO1067
	646	CR1063	680	CT750	714	CSS16	748	CO1069

	749	CO1080	783	DB257	817	CW1617	851	CT384
	750	CO1081	784	DB343	818	CW1632	852	CT392
	751	CO1094	785	DB415	819	CW1636	853	CT394
	752	CO956	786	DB53	820	CW1640	854	CT415
5	753	CO973	787	DB85	821	CW169	855	CT421
	754	CJ471	788	CW1000	822	CW172	856	CT423
	755	CJ472	789	CW1038	823	CW173	857	CT434
	756	CJ475	790	CW1087	824	CW175	858	CT440
	757	CJ483	791	CW1100	825	CV123	859	CT443
10	758	CJ484	792	CW1109	826	CV156	860	CT450
	759	CJ485	793	CW1112	827	CV160	861	CT453
	760	CJ486	794	CW1115	828	CV192	862	CT457
	761	CJ488	795	CW1150	829	CV203	863	CT466
	762	CJ496	796	CW1155	830	CV215	864	CT474
15	763	CJ497	797	CW1177	831	CV227	865	CT475
	764	CJ498	798	CW1195	832	CV263	866	CT479
	765	CJ507	799	CW1200	833	CV275	867	CT489
	766	CJ508	800	CW1201	834	CV305	868	CT51
	767	CJ519	801	CW1214	835	CV328	869	CT519
20	768	CJ520	802	CW1225	836	CV380	870	CT521
	769	CJ521	803	CW1230	837	CV394	871	CT526
	770	CJ522	804	CW1233	838	CV410	872	CT536
	771	CJ534	805	CW1272	839	CV416	873	CT541
	772	CJ536	806	CW1292	840	CV461	874	CT547
25	773	CJ543	807	CW1306	841	CV493	875	CT550
	774	CJ544	808	CW1311	842	CV501	876	CT559
	775	CJ547	809	CW1314	843	CT3	877	CT562
	776	CK53	810	CW1334	844	CT314	878	DE36
	777	CK7	811	CW1365	845	CT317	879	DE37
30	778	CK70	812	CW1372	846	CT320	880	DE4
	779	CL49	813	CW149	847	CT326	881	DE42
	780	CL63	814	CW152	848	CT340	882	DE63
	781	DB203	815	CW1574	849	CT353	883	DE70
	782	DB208	816	CW1611	850	CT358	884	DE83

	885	DE103	919	CS771	953	CW775	987	DA337
	886	DE105	920	CS773	954	CW795	988	DA348
	887	DE110	921	CS776	955	CW802	989	DA373
	888	DE114	922	CW222	956	CW823	990	DA388
5	889	DE117	923	CW224	957	CW835	991	DA389
	890	DE119	924	CW226	958	CZ115	992	DA390
	891	DE91	925	CW232	959	CZ122	993	DA391
	892	DE95	926	CW254	960	CZ186	994	DA414
	893	DE96	927	CW272	961	CZ214	995	DA428
10	894	CW420	928	CW280	962	CZ247	996	DA443
	895	CW424	929	CW313	963	CZ251	997	DA451
	896	CW457	930	CW314	964	CZ268	998	CW1458
	897	CW485	931	CW347	965	CZ270	999	CW1475
	898	CS383	932	CW354	966	CZ278	1000	CW1481
15	899	CS384	933	CW363	967	CZ291	1001	CW1506
	900	CS399	934	CW374	968	CZ320	1002	CW1510
	901	CS405	935	CW382	969	CZ326	1003	CW1543
	902	CS409	936	CW383	970	CZ362	1004	CW1550
	903	CS431	937	CW386	971	CW1414	1005	CW1552
20	904	CS438	938	CW388	972	CW1440	1006	CZ372
	905	CS454	939	CW512	973	CE209	1007	CZ374
	906	CS588	940	CW517	974	CE216	1008	CW902
	907	CS629	941	CW53	975	CE232	1009	CW922
	908	CS636	942	CW554	976	CE242	1010	CW924
25	909	CS637	943	CW585	977	CF193	1011	CW976
	910	CS638	944	CW618	978	CH776	1012	CW979
	911	CS645	945	CE197	979	CW1381	1013	CW984
	912	CS679	946	CW662	980	CW1389	1014	CW998
	913	CS682	947	CW675	981	CW1399	1015	CZ1
30	914	CS734	948	CW691	982	CZ653	1016	CW753
	915	CS743	949	CW707	983	CZ681	1017	CW759
	916	CS752	950	CW735	984	CZ711	1018	CW800
	917	CS756	951	CW762	985	CZ719	1019	CW891
	918	CS765	952	CW768	986	DA306	1020	CW960

	1021	CT80	1055	DC14	1089	DH1206	1123	DF478
	1022	DF1115	1056	CW1670	1090	DH1212	1124	DF483
	1023	DF1117	1057	CW1682	1091	DH1213	1125	DF494
	1024	DF1125	1058	DF814	1092	DH190	1126	DF499
5	1025	DF134	1059	DF821	1093	DI191	1127	DF7
	1026	DF14	1060	DF842	1094	DI207	1128	DF706
	1027	DF163	1061	DG1	1095	DI216	1129	DF713
	1028	DF174	1062	DG17	1096	DI243	1130	DF727
	1029	DF175	1063	DG174	1097	DI248	1131	DF737
10	1030	DF180	1064	DG256	1098	DI261	1132	DF756
	1031	DF185	1065	DG26	1099	DF1005	1133	DF757
	1032	DF201	1066	DG266	1100	DF1009	1134	DF762
	1033	DF202	1067	DG326	1101	DF1010	1135	DF776
	1034	DF203	1068	DG327	1102	DF102	1136	DF777
15	1035	DF206	1069	DG329	1103	DF1050	1137	DF780
	1036	DF219	1070	DG330	1104	DF1062	1138	DF783
	1037	DF230	1071	DG331	1105	DF1063	1139	DG12
	1038	DF232	1072	DG44	1106	DF1084	1140	DG121
	1039	DF239	1073	DG65	1107	DF153	1141	DG128
20	1040	DF244	1074	DG69	1108	DF218	1142	DG141
	1041	DF259	1075	DG7	1109	DF251	1143	DG149
	1042	DF266	1076	DG71	1110	DF280	1144	DH28
	1043	DF46	1077	DG76	1111	DF286	1145	DH303
	1044	DF65	1078	DG82	1112	DF316	1146	DH318
25	1045	DF69	1079	DH1086	1113	DF317	1147	DH322
	1046	DB145	1080	DH1098	1114	DF343	1148	DH340
	1047	DB150	1081	DH1135	1115	DF347	1149	DH371
	1048	DB159	1082	DH1145	1116	DF370	1150	DH40
	1049	DB174	1083	DH1153	1117	DF382	1151	DH401
30	1050	DB180	1084	DH1182	1118	DF396	1152	DH432
	1051	CY1	1085	DH1185	1119	DF428	1153	DH451
	1052	CY11	1086	DH1190	1120	DF453	1154	DH496
	1053	CY3	1087	DH1191	1121	DF457	1155	DH502
	1054	CY9	1088	DH1201	1122	DF460	1156	DH529

	1157	DH66	1191	DF915	1225	DH1357	1259	DI501
	1158	DF518	1192	DF948	1226	DH145	1260	DI504
	1159	DF521	1193	DF950	1227	DH999	1261	DK111
	1160	DF538	1194	DF956	1228	DI160	1262	DK113
5	1161	DF543	1195	DF966	1229	DI386	1263	DK120
	1162	DF545	1196	DF968	1230	DI391	1264	DK122
	1163	DF547	1197	DF971	1231	DI435	1265	DK126
	1164	DF568	1198	DF973	1232	DI448	1266	DK134
	1165	DF587	1199	DF979	1233	DI454	1267	DK136
10	1166	DF589	1200	DF984	1234	DJ109	1268	DK150
	1167	DF591	1201	DF989	1235	DJ146	1269	DK160
	1168	DF601	1202	DH1257	1236	DJ167	1270	DK170
	1169	DF606	1203	DH1308	1237	DF1065	1271	DK182
	1170	DF62	1204	DH1314	1238	DI387	1272	DK185
15	1171	DF620	1205	DI341	1239	DI393	1273	DK197
	1172	DF625	1206	DH1265	1240	DI403	1274	DK206
	1173	DF648	1207	DI349	1241	DI430	1275	DK219
	1174	DF657	1208	DI355	1242	DI438	1276	DK223
	1175	DF659	1209	DI362	1243	DJ2	1277	DK227
20	1176	DF661	1210	DI366	1244	DJ188	1278	DK229
	1177	DF662	1211	DI508	1245	DJ238	1279	DK230
	1178	DF670	1212	DI516	1246	DJ259	1280	DK243
	1179	DF674	1213	DI518	1247	DK64	1281	DK264
	1180	DF682	1214	DF1066	1248	DK70	1282	DK268
25	1181	DF688	1215	DF1069	1249	DK81	1283	DK31
	1182	DF810	1216	DG279	1250	DK84	1284	DK39
	1183	DF823	1217	DH1010	1251	DI462	1285	DK93
	1184	DF835	1218	DH1013	1252	DI466	1286	DL101
	1185	DF860	1219	DH1044	1253	DI474	1287	DL110
30	1186	DF877	1220	DH1045	1254	DI475	1288	DL116
	1187	DF883	1221	DH1073	1255	DI479	1289	DL132
	1188	DF895	1222	DH1078	1256	DI480	1290	DL63
	1189	DF909	1223	DH1340	1257	DI482	1291	DL82
	1190	DF910	1224	DH1349	1258	DI500	1292	DL95

	1293	DL99	1327	DL491	1361	DL547	1395	DO181
	1294	DJ332	1328	DL495	1362	DL550	1396	DO419
	1295	DJ362	1329	DL498	1363	DL551	1397	DO424
	1296	DK290	1330	DL504	1364	DL601	1398	DO440
5	1297	DK321	1331	DM118	1365	DL604	1399	DO447
	1298	DK324	1332	DM122	1366	DL605	1400	DO568
	1299	DK329	1333	DM126	1367	DL607	1401	DO575
	1300	DK357	1334	DM128	1368	DL608	1402	DO589
	1301	DK360	1335	DM130	1369	DL616	1403	DO610
10	1302	DL141	1336	DM147	1370	DL619	1404	DO715
	1303	DL146	1337	DM169	1371	DL620	1405	DO722
	1304	DL162	1338	DM26	1372	DL634	1406	DO737
	1305	DL163	1339	DM404	1373	DM194	1407	DO742
	1306	DL169	1340	DM406	1374	DM197	1408	DO755
15	1307	DL181	1341	DM407	1375	DM221	1409	DO765
	1308	DL185	1342	DM420	1376	DM248	1410	DO797
	1309	DL218	1343	DM425	1377	DM250	1411	DO836
	1310	DL220	1344	DM435	1378	DM262	1412	DO884
	1311	DL248	1345	DM445	1379	DM265	1413	DO896
20	1312	DL289	1346	DM449	1380	DM272	1414	CZ549
	1313	DL290	1347	DM459	1381	DM278	1415	CZ598
	1314	DL291	1348	DM462	1382	DM293	1416	DT431
	1315	DL316	1349	DM469	1383	DM303	1417	DT443
	1316	DL320	1350	DM482	1384	DM340	1418	DT446
25	1317	DL321	1351	DM6	1385	DM360	1419	DT449
	1318	DL425	1352	DM94	1386	DM365	1420	DT450
	1319	DL426	1353	DJ279	1387	DM522	1421	DT455
	1320	DL427	1354	DJ284	1388	DM533	1422	DT458
	1321	DL439	1355	DJ299	1389	DM542	1423	DN106
30	1322	DL440	1356	DJ319	1390	DM87	1424	DN153
	1323	DL444	1357	DJ323	1391	DN124	1425	DN176
	1324	DL457	1358	DL531	1392	DN144	1426	DT530
	1325	DL463	1359	DL535	1393	DN147	1427	DT534
	1326	DL466	1360	DL543	1394	DN167	1428	DT535

	1429	DT544	1463	DW1	1497	BKS
	1430	DT563	1464	DW389	1498	BK504
	1431	DT584	1465	DW398	1499	BK513
	1432	DT590	1466	DW654	1500	BK517
5	1433	DT596	1467	DW659		
	1434	DT597	1468	DW665		
	1435	DT598	1469	DW694		
	1436	DT640	1470	DW705		
	1437	DT655	1471	DW716		
10	1438	DT674	1472	DW749		
	1439	DT719	1473	DW761		
	1440	DT734	1474	DW765		
	1441	DT779	1475	DW771		
	1442	DT801	1476	DW78		
15	1443	DT802	1477	DW780		
	1444	DN696	1478	BK10		
	1445	DN697	1479	BK11		
	1446	DN704	1480	BK2		
	1447	DN710	1481	BK368		
20	1448	DN711	1482	BK373		
	1449	DN714	1483	BK374		
	1450	DN721	1484	BK375		
	1451	DN722	1485	BK384		
	1452	DN732	1486	BK402		
25	1453	DN740	1487	BK410		
	1454	DN746	1488	BK415		
	1455	DN747	1489	BK425		
	1456	DN753	1490	BK427		
	1457	DN756	1491	BK436		
30	1458	DN764	1492	BK445		
	1459	DN770	1493	BK455		
	1460	DN772	1494	BK458		
	1461	DN1120	1495	BK494		
	1462	DU372	1496	BK498		

The "Clone ID No." for a particular clone consists of one or two letters followed by a number. The letters designate the tissue source from which the sEST was isolated. Table 3 below lists the various sources which were run through applicants' signal sequence trap. Thus, the tissue source for a particular sEST sequence can be identified in Table 3 by the 5 one and two letter designations used in the relevant "Clone ID No.". For example, a clone designated as "BA312" would have been isolated from a human placenta (26 yrs.) library (i.e., selection "BA") as indicated in Table 3.

As used herein, "polynucleotide" includes single- and double-stranded RNAs, DNAs and RNA:DNA hybrids.

10 As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins 15 which are transported across the membrane of the endoplasmic reticulum.

20 Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are 25 incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also 30 be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

35 The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or other host cell. The sequence of the mature form of the protein may also be determinable from the amino acid sequence of the full-length form.

The present invention also provides genes corresponding to the cDNA sequences disclosed herein. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification 5 and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials.

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that 10 the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. Species homologs may be isolated and identified by making 15 suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous or related to that encoded by the 20 polynucleotides disclosed herein.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides capable of hybridizing, preferably under reduced stringency conditions, more preferably under stringent conditions, 25 most preferably under highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in Table 1 below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Table 1

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	< 50	T _B *; 1xSSC	T _B *; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	< 50	T _D *; 1xSSC	T _D *; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	< 50	T _F *; 1xSSC	T _F *; 1xSSC
	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	< 50	T _H *; 4xSSC	T _H *; 4xSSC
10	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	< 50	T _J *; 4xSSC	T _J *; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	< 50	T _L *; 2xSSC	T _L *; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	< 50	T _N *; 6xSSC	T _N *; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	< 50	T _P *; 6xSSC	T _P *; 6xSSC
20	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	< 50	T _R *; 4xSSC	T _R *; 4xSSC

¹: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

* $T_B - T_R$: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5–10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(\text{°C}) = 2(\# \text{ of A + T bases}) + 4(\# \text{ of G + C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(\text{°C}) = 81.5 + 16.6(\log [\text{Na}^+]) + 0.41(\% \text{G+C}) - (600/N)$, where N is the number of bases in the hybrid, and $[\text{Na}^+]$ is the concentration of sodium ions in the hybridization buffer ($[\text{Na}^+]$ for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, such hybridizing polynucleotides have at least 70% sequence identity (more preferably, at least 80% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which they hybridize, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps. The isolated polynucleotide encoding the protein of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, Nucleic Acids Res. 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control

sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

5 A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

10 Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any 15 bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

20 The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, 25 as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

30 The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (i.e., from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl or Cibacrom blue 3GA

Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which 5 will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently 10 purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or 15 all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic 20 animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are 25 known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological 30 processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modifications are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications

of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, 5 replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening 10 or other immunological methodologies may also be easily made by those skilled in the art given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

USES AND BIOLOGICAL ACTIVITY

The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention 5 may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

10 The polynucleotides provided by the present invention can be used by the research community for various purposes. The primary use of polynucleotides of the invention which are sESTs is as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond (i.e., is a longer polynucleotide sequence of which substantially the entire sEST is a fragment in the case of a full-length cDNA, or 15 which encodes the sEST in the case of a genomic DNA molecule) to such sESTs. Techniques for use of such sequences as probes for larger cDNAs or genomic molecules are well known in the art.

The polynucleotides can also be used to express recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding 20 protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related 25 DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti- 30 DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify

polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more 5 factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

10 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-15 Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

20 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon γ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 25 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current 30 Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; DeVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley

and Sons, Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991; Measurement of mouse and human Interleukin 9 -

5 Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in:

10 Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 15 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may 20 be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, 25 in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre

syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other 5 conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune 10 response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from 15 immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7)), e.g., preventing 20 high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys 25 the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the 30 molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this manner prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-

blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, *Science* 257:789-792 (1992) and Turka *et al.*, *Proc. Natl. Acad. Sci. USA*, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., *Fundamental Immunology*, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral

infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient

5 by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding

10 a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably

15 B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor

20 cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection

25 *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or

30 which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I

or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected 5 with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured 10 by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro assays for Mouse Lymphocyte Function 3.1-15 3.19*; Chapter 7, *Immunologic studies in Humans*); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; 20 Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; 25 Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching 25 (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro antibody production*, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

30 Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, *In Vitro assays for Mouse Lymphocyte Function 3.1-*

3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Takai et al., *J. Immunol.* 140:508-512, 1988; Bertagnolli et al., *J. Immunol.* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., *J. Immunol.* 134:536-544, 1995; Inaba et al., *Journal of Experimental Medicine* 173:549-559, 1991; Macatonia et al., *Journal of Immunology* 154:5071-5079, 1995; Porgador et al., *Journal of Experimental Medicine* 182:255-260, 1995; Nair et al., *Journal of Virology* 67:4062-4069, 1993; Huang et al., *Science* 264:961-965, 1994; Macatonia et al., *Journal of Experimental Medicine* 169:1255-1264, 1989; Bhardwaj et al., *Journal of Clinical Investigation* 94:797-807, 1994; and Inaba et al., *Journal of Experimental Medicine* 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

20 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

25 Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for

example, in conjunction with chemotherapy to prevent or treat consequent myelosuppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet 5 transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post 10 irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., 20 *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; 25 30 Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland,

H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

5 A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

10 A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma 15 induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

20 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

25 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein 30 may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. *De novo* tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic

plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or 5 progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural 10 cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized 15 neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from 20 chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

25 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of 30 fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

5 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

10 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, *J. Invest. Dermatol* 71:382-84 (1978).

15 **Activin/Inhibin Activity**

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, 20 alone or in heterodimers with a member of the inhibin α family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- β group, may 25 be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

30 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale

et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

5 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide
10 particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

15 A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

20 The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one
25 cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et
30 al. *APMIS* 103:140-146, 1995; Muller et al *Eur. J. Immunol.* 25: 1744-1748; Gruber et al. *J. of Immunol.* 152:5860-5867, 1994; Johnston et al. *J. of Immunol.* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A 5 protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

10 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., *J. Clin. Pharmacol.* 26:131-140, 1986; Burdick et al., *Thrombosis Res.* 45:413-419, 1987; Humphrey et al., *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

15 **Receptor/Ligand Activity**

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors 20 involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. 25 A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those 30 described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., *Proc. Natl. Acad. Sci. USA* 84:6864-6868, 1987; Bierer et al., *J. Exp. Med.* 168:1145-1156, 1988; Rosenstein et al., *J. Exp. Med.*

169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,
Cell 80:661-670, 1995.

Anti-Inflammatory Activity

5 Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or 10 suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, 15 arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

20 **Tumor Inhibition Activity**

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor 25 precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

30

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting

(suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the 5 fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent 10 behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for 15 example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

ADMINISTRATION AND DOSING

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a 5 composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the 10 invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or 15 use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects 20 of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical compositions of the invention may comprise a protein of the invention in such multimeric 25 or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T 30 lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that

can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

5 The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, 10 diglycerides, sulfatides, lyssolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

15 As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, 20 administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

25 In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either 30 simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous 5 administration to the patient is preferred.

When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an 10 adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain 15 physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

20 When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical 25 composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, 30 antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with

which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is 5 contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 μ g to about 100 mg (preferably about 0.1 ng to about 10 mg, more preferably about 0.1 μ g to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the 10 present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the 15 pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide immunogens additionally may contain a cysteine residue at the carboxyl terminus, 20 and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer. Chem. Soc. 85, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. 211, 10 (1987). Monoclonal antibodies binding to the protein of the invention may be useful diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal 25 antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the 30 protein.

For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systematically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a

pyrogen-free, physiologically acceptable form. Further, the composition may desirably be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also 5 optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and 10 cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices 15 for the compositions may be biodegradable and chemically defined calcium sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such 20 as sintered hydroxapatite, bioglass, aluminates, or other ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

25 Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions from disassociating from the matrix.

30 A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropyl-methylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate,

poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to provide appropriate handling of 5 the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in 10 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- α and TGF- β), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to humans, are desired 15 patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of a wound, type 20 of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect the dosage. Progress 25 can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other 30 known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.

Table 3

Sel.	Species	Tissue	Cell Type
AA	Human	Kidney	19-23wks., M/F pool of 5
AB	Human	Fetal Lung	Fetal Lung
AC	Human	Placenta	26yrs., 1 specimen
AD	Murine	Embryo	Fetal ES cells
AE	Murine	Spleen	Adult spleen
AF	Murine	Fetal Brain	Fetal Brain
AG	Murine	Fetal Brain	Fetal Brain
AH	Murine	Fetal Thymus	Fetal Thymus
AI	Human	Blood	Adult PBMC/TH1or2
AJ	Human	Testes	10-61yrs., pool of 11
AK	Human	Kidney	19-23wks., M/F pool of 5
AL	Human	Neural	Adult Glioblastoma line TG-1
AM	Human	Kidney	19-23wks., M/F pool of 5
AN	Murine	Bone Marrow	Adult Stromal cell line FCM-4
AO	Murine	Thymus	Adult Subtr. Adult Thymus
AP	Human	Placenta	26yrs., 1 specimen
AQ	Human	Ovary	PA-1 Teratocarcinoma
AR	Human	Retina	16-75yrs., pool of 76
AS	Human	Brain	19-23wks., M/F pool of 5
AT	Human	Blood	Adult lymphocytes+dend. cells
AU	Human	Testes	10-61yrs., pool of 11
AV	Murine	Spleen	Adult spleen
AW	Human	Ovary	PA-1 Teratocarcinoma
AX	Human	Testes	10-61yrs., pool of 11
AY	Human	Retina	16-75yrs., pool of 76
AZ	Human	Colon	Caco-2 Adenocarcinoma
B	Human	Blood	PeripheralBloodMononuclearCell
BA	Human	Placenta	26yrs., 1 specimen
BB	Human	Blood	Adult PBMC/TH1or2
BC	Murine	Embryo	Fetal ES cells
BD	Human	Kidney	19-23wks., M/F pool of 5
BE	Human	Blood	Adult PBMC/TH1or2
BF	Human	Brain	19-23wks., M/F pool of 5
BG	Human	Brain	N/A
BH	Human	Ovary	PA-1 Teratocarcinoma
BI	Human	Kidney	19-23wks., M/F pool of 5
BJ	Human	Ovary	PA-1 Teratocarcinoma
BK	Human	Retina	16-75yrs., pool of 76
BL	Human	Testes	10-61yrs., pool of 11
BM	Human	Muscle	N/A
BN	Human	Placenta	26yrs., 1 specimen
BO	Human	Retina	16-75yrs., pool of 76
BP	Human	Kidney	19-23wks., M/F pool of 5
BQ	Human	Colon	Caco-2 Adenocarcinoma Caco2

BR	Human	Kidney	19-23wks., M/F pool of 5
BS	Human	Pituitary	Adult Pituitary
BT	Human	Blood	Adult PBMC
BU	Human	Placenta	26yrs., 1 specimen
BV	Human	Brain	N/A
BW	Human	Blood	Adult PBMC
BX	Human	Ovary	PA-1 Teratocarcinoma
BY	Human	Blood	Adult PBMC/TH1or2
BZ	Human	Kidney	19-23wks., M/F pool of 5
C	Human	Blood	PeripheralBloodMononuclearCell
CA	Murine	Embryo	Fetal ES cell embryoid bodies
CB	Human	Brain	19-23wks., M/F pool of 5
CC	Human	Brain	N/A
CD	Human	Brain	19-23wks., M/F pool of 5
CE	Human	Blood	Adult lymphocytes+dend. cells
CF	Human	Placenta	26yrs., 1 specimen
CG	Human	Testes	10-61yrs., pool of 11
CH	Human	Kidney	19-23wks., M/F pool of 5
CI	Human	Brain	N/A
CJ	Human	Brain	19-23wks., M/F pool of 5
CK	Human	Testes	10-61yrs., pool of 11
CL	Human	Retina	16-75yrs., pool of 76
CM	Human	Adult Lung	Adult Lung
CN	Human	Brain	19-23wks., M/F pool of 5
CO	Human	Brain	N/A
CP	Human	SalivaryGland	N/A
CQ	Human	Heart	13-73yrs., pool of 3
CR	Human	Testes	10-61yrs., pool of 11
CS	Human	Brain	19-23wks., M/F pool of 5
CT	Human	Brain	N/A
CU	Human	Pineal Gland	N/A
CV	Human	Mammary	Adult Human Mammary
CW	Human	Brain	19-23wks., M/F pool of 5
CY	Human	Pineal Gland	N/A
CZ	Human	Testes	10-61yrs., pool of 11
D	Human	Blood	PeripheralBloodMononuclearCell
DA	Human	Placenta	26yrs., 1 specimen
DB	Human	Prostate	Adult Prostate
DC	Human	Pineal Gland	Adult Pineal Gland
DD	Human	Testes	10-61yrs., pool of 11
DE	Human	Testes	Adult NCCIT TeratoCA
DF	Human	Brain	N/A
DG	Human	Placenta	26yrs., 1 specimen
DH	Human	Brain	19-23wks., M/F pool of 5
DI	Human	Testes	10-61yrs., pool of 11
DJ	Human	Placenta	26yrs., 1 specimen
DK	Human	Fetal Kidney2	Fetal Kidney

DL	Human	Brain	N/A
DM	Human	Brain	N/A
DN	Human	Brain	19-23wks., M/F pool of 5
DO	Human	Testes	10-61yrs., pool of 11
DP	Murine	Embryo	Fetal ES cell embryoid bodies
DQ	Human	Placenta	26yrs., 1 specimen
DR	Human	SalivaryGland	N/A
DT	Human	Brain	N/A
DU	Human	Brain	19-23wks., M/F pool of 5
DV	Human	Pineal Gland	Adult Pineal Gland
DW	Human	Brain	N/A
DX	Human	Testes	10-61yrs., pool of 11
DY	Human	Brain	N/A
DZ	Human	Testes	Adult NCCIT TeratoCA
E	Human	Blood	PeripheralBloodMononuclearCell
EA	Human	Brain	19-23wks., M/F pool of 5
EB	Human	Melanoma	Adult Melanoma
EC	Human	Brain	N/A
ED	Human	Placenta	26yrs., 1 specimen
EE	Human	Testes	10-61yrs., pool of 11
EF	Human	Liver	Adult Liver
EG	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
EH	Human	Blood	PeripheralBloodMononuclearCell
EI	Human	Brain	19-23wks., M/F pool of 5
EJ	Human	Placenta	26yrs., 1 specimen
EK	Human	Brain	19-23wks., M/F pool of 5
EL	Human	Testes	10-61yrs., pool of 11
EM	Human	Fetal Kidney2	Fetal Kidney
EN	Human	Brain	19-23wks., M/F pool of 5
EO	Human	Adrenal Gland	Adult Adrenal Gland
EP	Human	Placenta	26yrs., 1 specimen
EQ	Human	Testes	10-61yrs., pool of 11
ER	Human	Brain	19-23wks., M/F pool of 5
ES	Human	Placenta	26yrs., 1 specimen
ET	Human	Testes	10-61yrs., pool of 11
EU	Human	Kidney	Adult Kidney
EV	Human	Stomach	Adult Stomach
EW	Human	Placenta	26yrs., 1 specimen
EX	Human	Testes	10-61yrs., pool of 11
EY	Human	Brain	19-23wks., M/F pool of 5
EZ	Human	Fetal Kidney2	Fetal Kidney
FA	Human	Brain	19-23wks., M/F pool of 5
FB	Human	Placenta	26yrs., 1 specimen
FC	Human	Testes	10-61yrs., pool of 11
FD	Human	SalivaryGland	N/A
FE	Human	Brain	N/A
FF	Human	Testes	Adult NCCIT TeratoCA

FG	Human	Brain	N/A
FH	Human	Brain	19-23wks., M/F pool of 5
FI	Human	Small Intest	Adult Small Intestine
FJ	Human	Lung CA	Adult Lung CA
FK	Human	Kidney	Adult Kidney
FM	Human	Brain	N/A
FN	Human	Brain	19-23wks., M/F pool of 5
FO	Human	Brain	N/A
FP	Human	Placenta	26yrs., 1 specimen
FQ	Human	Testes	10-61yrs., pool of 11
FR	Human	Placenta	26yrs., 1 specimen
FS	Human	Testes	10-61yrs., pool of 11
FT	Chicken	Fetal Lung	Fetal Lung
FU	Chicken	Limb Bud	Fetal St. 23 Limb Bud
FV	Human	Testes	Adult NCCIT TeratoCA
FW	Human	Testes	Adult NCCIT TeratoCA
FX	Human	Brain	19-23wks., M/F pool of 5
FY	Human	Placenta	26yrs., 1 specimen
FZ	Human	Placenta	26yrs., 1 specimen
G	Human	Blood	PeripheralBloodMononuclearCell
GA	Human	Testes	10-61yrs., pool of 11
GB	Human	Placenta	26yrs., 1 specimen
GC	Human	Testes	10-61yrs., pool of 11
GD	Human	Placenta	26yrs., 1 specimen
GE	Human	Brain	N/A
GF	Human	Brain	19-23wks., M/F pool of 5
GG	Human	Fetal Kidney2	Fetal Kidney
GH	Human	Placenta	26yrs., 1 specimen
GI	Human	Retinoblastoma	Adult Retinoblastoma Y79
GJ	Murine	Spleen	Adult Spleen
GK	Human	Fetal Kidney2	Fetal Kidney
GL	Murine	Lymph Node	Adult Lymph Node
GM	Human	Uterus	N/A
GN	Human	Blood	PeripheralBloodMononuclearCell
GO	Human	Adrenal Gland	Adult Adrenal Gland
GP	Human	Ovary	PA-1 Teratocarcinoma
GQ	Human	Pineal Gland	N/A
GR	Human	Pancreas	Adult HPC-3 Ductal AdenoCA
GS	Human	Retina	16-75yrs., pool of 76
GT	Human	Brain	N/A
GU	Human	Fetal Kidney2	Fetal Kidney
GV	Rat	Retina	Newborn Retina
GW	Chicken	Limb Bud	Fetal St.26 Limb Bud
GX	Human	Brain	N/A
GY	Human	Testes	10-61yrs., pool of 11
GZ	Human	Brain	19-23wks., M/F pool of 5
H	Human	Blood	PeripheralBloodMononuclearCell

HA	Human	Testes	Adult NCCIT TeratoCA
HB	Human	Fetal Kidney2	Fetal Kidney
HC	Human	Brain	19-23wks., M/F pool of 5
HD	Human	Brain	N/A
HE	Human	Testes	10-61yrs., pool of 11
HF	Human	Brain	19-23wks., M/F pool of 5
HG	Human	Fetal Kidney2	Fetal Kidney
HH	Human	Brain	N/A
HI	Human	Testes	10-61yrs., pool of 11
HJ	Human	Brain	N/A
HK	Human	Brain	19-23wks., M/F pool of 5
HL	Human	Fetal Kidney2	Fetal Kidney
HM	Human	Testes	Adult NCCIT TeratoCA
HN	Human	Fetal Kidney2	Fetal Kidney
HO	Human	Brain	N/A
HP	Human	Brain	19-23wks., M/F pool of 5
HQ	Human	Testes	10-61yrs., pool of 11
HR	Human	Brain	N/A
HS	Human	Brain	N/A
HT	Human	Brain	19-23wks., M/F pool of 5
HU	Human	Fetal Kidney2	Fetal Kidney
HV	Human	Testes	10-61yrs., pool of 11
HW	Human	Brain	N/A
HX	Human	Brain Hippoca	Adult Brain Hippocampus
HY	Human	Trachea	Adult Trachea
HZ	Human	Brain Thalamus	Adult Brain Thalamus
I	Human	Blood	PeripheralBloodMononuclearCell
IA	Human	Thyroid	Adult Thyroid
IB	Human	Embryonal CA	Fetal NT2-D1
IC	Human	WER1-Rb1 line	Adult Retinoblastoma
ID	Human	Muscle	N/A
IE	Human	Brain	19-23wks., M/F pool of 5
IF	Human	Uterus	N/A
IG	Human	Testes	10-61yrs., pool of 11
IH	Human	Muscle	N/A
II	Human	Brain	N/A
IJ	Human	Blood	PeripheralBloodMononuclearCell
IK	Human	Retinoblastoma	Adult Retinoblastoma Y79
IL	Human	Retina	16-75yrs., pool of 76
IM	Human	Various	Various
IN	Human	Prostate	Adult Prostate
IO	Human	Brain	19-23wks., M/F pool of 5
IP	Human	Fetal Kidney2	Fetal Kidney
IQ	Human	Prostate	Adult Prostate
IR	Human	Brain Hippoca	Adult Brain Hippocampus
IS	Human	Trachea	Adult Trachea
IT	Human	Brain Thalamu	Adult Brain Thalamus

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jacobs, Kenneth
 McCoy, John
 LaVallie, Edward
 Racie, Lisa
 Merberg, David
 Treacy, Maurice
 Spaulding, Vikki
 Agostino, Michael

(ii) TITLE OF INVENTION: SECRETED, EXPRESSED SEQUENCE TAGS

(iii) NUMBER OF SEQUENCES: 1500

(iv) CORRESPONDENCE ADDRESS

(A) ADDRESSE: Genetics Institute, Inc.
 (B) STREET: 87 CambridgePark Drive
 (C) CITY: Cambridge
 (D) STATE: Massachusetts
 (E) COUNTRY: U.S.A
 (F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy Disk
 (B) COMPUTER: IBM PC Compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.
 (B) REGISTRATION NUMBER: 32,724

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 498-8224
 (B) TELEFAX: (617) 876-5851

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCTGGCC TTCATGGCCT AAGTGTAA ATTATAAGCT GGTGAAGTGA AATAACACAA	60
ATCAAGCTCA CCAATTAA TACTCAGCTG TTGATAAACAA ACACGAAGA GTGACATTTA	120
AATTGAATT ATCTTCTTTG AAGTAGCATT GCAGCACTT TGAATGACTT CAAAAGGCT	180
GATCATAAAA ATCACTCAA TCATTTCAA ATTTTACTTT AGCAGCAATG AAGTTATTC	240

GTATGACTCA GATGAACCTT CTGCTCTGTC TTGGAGTTAT TATGGTCATT TCATTTCTG	300
CAACCTGGGA AAACCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAATTCGGCC TTCAATGGCCT ACGAGTGGAT CTGGTTGAGA GGAAAGCAGC TAAAAATACA	60
GGAGATGAAA GGGATCATAA CGAACATAAT GAACCATGTT CATTATGGTT CGTGGGGAGG	120
CAGGAAAGCA CAGTATCCAG GGCATAGGCAGAAGAGCTGT CTTTACCGGG AGGAGGGAA	180
CATATTCTAC TGCAATAAGC AAGGGCGGGG TAAGTACCGA TCGGGTACTT TGGGAACATAT	240
GACGGTAGGG AGTCAGGAA GTTGCTGCCT GAAGGCATAA AGGTTTTTTT TTTTTTTTT	300
TTTTTTTGCC AATTGGTCCA GTACCCCTCCT TCTGTGGCCC CCATCTCCAG TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAATTCTTTA TATAATTTGG ATACCTACTC ATTGTCAGTT GTATGCTTTG CAAATATCTT	60
TCCTGACCCCT TACTTACCTT TTCACTCTTA ATGGTATCTT TGATGAATCA AAAATTTTC	120
TTTTTTGTT GTTTTTGAG ACAGAGCTTT AACTCTGTCA CCCAGGCTGG AGTGCAGTGC	180
ATGAACATGG CTCACTGCAG CCTCAACTTC TTGGACTCAA GCAATCCTCC TGCCCTCAGAA	240
CCTCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GAATTCGGCC TTCATGGCCT AGACCTGCCT CTAGCTCCTT TCCTTCTACT CTCCTGCTCA	60
GACCATTAGT AGGTACTTTG TAAATAAAAA AACTAGATTA ACATCAATAT TACTCCAATT	120
TGGTATCTTT TACACTATGT ATTATACCTA CTTCTTTT ATTTCATTAA CAAATAGTTT	180
AAATTACTTT ATCAAACCGAGC TGTATTGTTT CCCTCTTGTAA AAAGTACCAT CAAAGTGGGA	240
AAATGTATGT GGCACTCTCG AG	262

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGCC	TTCATGGCCT	AATAACTTAC	CCAGTCACGA	ATATTTCTTC	ATAGCAGCAT	60
CAGAGTGGAC	TAATACGATT	ATAATTATCA	TCACCTTTG	ACTGACCAAT	TGATTTACAG	120
TATTGAGTTC	AATCTGTTTT	TTTAAAAAAAT	ATCTTCTAAA	TATCAGGTGC	TGTATTAGAT	180
GTGGGGTACA	AAAATGTATT	TTCATTTACT	CACTAATTAA	CTTAAAATTT	ATTTATTGAG	240
GTACCTCGAG						250

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GAATTCCGGCC	TTCATGGCCT	AGGTGCTCGA	AGTAAGCTGT	GTGAACAAAT	GAGACGATTG	60
CCCTTTCTAA	TGAGTTTATA	TGCAATGTGG	TATCTTTACC	GATACATGCT	CTGTCAGAAA	120
GAAGCAGCCCC	ACTTCTGTCC	AATAGCCAAT	CCGGCTTCAG	GAGCAGCAGG	AGAGGCTTCG	180
GGAACGGGAG	AAGAGGCTTC	AGCAGCTGGC	CGAGCCACAG	AGCAGACTTGG	AGGAGCTGCA	240
CGAGAACAAAG	AGCGCACTGC	AGTTGGAGAG	CTCGAG			276

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAATTCCGGCC	TTCATGGCCT	ACTCATTCCA	AAATAAAAAA	AAAATTTCC	CATGATCTTA	60
TCTAGCTTCT	CTAGCAGTAC	TTGTATGATT	TCACCTTTCT	TTCTTTATTC	TTTTCTTCCA	120
TATTTTTTTT	TTTGAGACA	GGGTCTCACT	CTATTGTCCA	GGCTAGAGTG	CAGTAGTTTG	180
ATCATGACTC	ACTCTAACCT	GGACCTCCGG	GGCCTAAGTA	ATCTTCCCAC	CTCAGCCTCT	240
CAAGTAGCTG	GGACTACAGG	GATGTACCAAC	CATGCCTGGC	TAAG		284

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGAATTCT AGACCTGCCT CGAGGACGCC	AGGGAAAGTGA	GTTGAAAATC	TGAAAATGCG	60
GCCATGGACT CGTTCCTGGC	GTGGATTAT	GCTCATCTT	TTTGCCCTGG	120
GTTTATATA CGTGGTCACT	TGGTACGAGA	TAATGACCAT	CCTGATCACT	180
ACTGTCCAAG ATTCTGGCAA	AGCTTGAACG	CTTAAACAG	CAGAATGAAG	240
AATGGCCGAA TCTCTCCGGA	TACCAAGG	CCCTATTGAT	CAGGGCCAG	300
AGTGCCTGTT	TTAGAAGAGC	AGCTTGTAA	GGCCAAAGAA	360
ACAGACCAGA	AATGGTCTGG	GGAGGATCT	CGAG	394

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCTGTGATGA AAATGCTTTA	TGCTTCAACA	CTGTTGGAGG	ACACAACGT	GTTTGCAGC	60
CGGGCTATAC AGGGAATGGA	ACGACATGCA	AAGCATTG	CAAAGATGGC	TGTAGGAATG	120
GAGGAGCCTG	TATTGCGCT	AATGTGTG	CCTGCCACA	AGGCTTCAGT	180
GTAACACGGA	CATIGATGAA	TGCTCTGATG	GTTTGTCA	ATGTGACAGT	240
GCATTAACCT	GCCTGGATGG	TACCACTGTG	AGTGCAGAGA	TGGCTACCAT	300
TGTTTCACC	AACTGGAGAA	TCGTGTGAAG	ATATTGATGA	GTGTGGGACC	357

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GAATTGGGCC TTCATGGCCT	ATTCGGATC	TATGTATCTG	TACTCATACA	GCCTCATCGG	60
GCTAAACAGC	CTTCTTTCA	GAACAGTAGA	TCACTCACT	GGGTTTCAA	120
ACCTTCAAG	GCTGGCTTTA	TAGGTCTTGC	CTCACTGTAT	CCAGCAATCC	180
CTATCCCAGT	CAGGACTGCA	CACCTCATAT	TGAAAGACAT	ACCTTAAAC	240
AAACCTTACA	AATATCCCAC	CCTTGACTCC	CGTTCTCGAG	CAGACTCCCC	280

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCTAGA CCTGCCTCGA GGCCACACA GTGACTGCCG GGTAAAGTTG TGGAATTACG	60
TCCCTGGACT CACCCCTG C TTCCCTGCC GAGTCCTGGC CATAAAGGGC CGCGCCACCA	120
CCCTGCCCTG ACCCTCCCCA ACTCTCCCTG TCTCCCTTT CATTCTTCCC CTCTTCCCT	180
TTCCCTCTCT TTCCCCACTT CGATATGAGC TGCTTCTTAA CGGTATGAGA TTATTTNACT	240
CCTTCTTCTT CCTTCCCTT CCTGTCTGC CTGGCTAGA GAGGTGCCCT GCCTGTCCCT	300
CCTGCACCCA CGTCCTTT CCAAGCATGA ACAGTGGGAC AGGCCCCAGG AGATGGGTGC	360
CAGGGAGCAG AAGGGGGAGC CTTCAGGCCT GGACAAAACG AAACACCCCC CCAAAAAAAAG	420
NAAACCCACG ACTCGAG	437

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTTCCTTCTA AGTAGATCTT CCTTCCCCAT TAAACTAGGT TTTCTACTGTC AAGATATTTT	60
GTGCAATTGCT GTTTAAACC CTTTTAACAG CGAACATAG CAGTCTAAGA AGTCTTCTGA	120
ACCATCCTGG ACTCTGGTG TGATTTAAA TTGTGTCTAC AAGTTCTCTG ACATTCTTCC	180
CACCAAGAGG TAGAGTCTGT TTCCCTCTCC TTTGAACCTA GGTAGGCCTT TGTTACTGCC	240
TTGATGAATA CAATGAGACT CGAG	264

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GATTTTTAC CCAAAGCTCT GGAATTGTAC ATTTATTTT TAAACTCAA AGAGGGAAAG	60
AGCCTTGTAT CATATGTGAA CATTGTATCA TAGGTAATGT TGTACAGACC CTTTTATACA	120
GTGATCTGTC TTGTTCTG C AGCAAAATC CTCTATGGAC ATAGGAGGTG CTGTGTCCCA	180
TGCCCTCTTG CCCTGACAGT GTCCCATGGG CCCCTTCTG CTCCCTGCC CCTCCCTGCT	240
ACTGCTGATG CACTCCCCC CCTCGAG	267

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAATTCCGCC	TTCATGGCCT	ATTTTTATT	TGTTTTGTTT	TGTTTTGTGG	GGATGGGCTT	60
TTGCCGTGTT	GCCCAGGCTG	GTTTCAATT	TTTGGGCTTA	TGCAATCCAC	CCACCTTGGC	120
CTCCCCAAAGT	GCAGGGATTA	CAGGCATGAG	CCATCTTGCT	GGGCACCTT	TTTCTTCTCT	180
TTTAACAAAT	TCAGCAATT	TTCAGTCCCA	GAATCTGTA	AATACATT	TTGTGGAAAA	240
ATACAATGGG	AATGGCATCA	AAAGATGGTT	TCTATTAGGA	ATGGAACAG	GTAACAGTTT	300
TCCCTGCCAC	CTCAACAATC	TCGAG				325

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGGCTGGCAG	GCGGGCCAAA	GGTAATGAAG	CAAAGAGAGA	GGGAAAAGAC	GTGTGAAAAT	60
TGCAGAGGGG	GTGACCGAGG	GAAACACGTG	AGCGTGTATA	TGACAGAAAA	ACCACGGAAG	120
GAGCAAACCT	GGGAGGGGG	TGGAAACCC	GGGCCGTTTC	CAGGGAGCAC	AGGCAGACTC	180
AGAGGTAACA	CTCAAAAGCA	ACAACAGAAG	CAAGGAGGAA	GTGGAAAAT	ATTTTTAATG	240
TGCTACAACG	AAACAGCTGC	CTGAATTCTA	TATACCTCT	GAAAATAATC	TGCACATAAA	300
ATGGGAAAGC	TTCACCGCAG	CAGACCCAC	TCGAG			335

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCGCC	TTCATGGCCT	ATGCTTCTTC	CACGCACCAAC	CACCAACCAC	ACCACCATCA	60
TGGCCATAGC	CACGGTGGCC	TGGGGGTGCT	GCCTGATGGG	CAGTCCAAGC	TCCAGGCCCT	120
GCATGCCAG	TATTGCAAG	GACCGGGCCC	TGCCCCGCCA	CCCTACCTCC	CACCCCAGCA	180
GCCCTCTCTT	CCCCCACCTC	CCCAGCAGCC	CCCACCCCTG	CCCCACCTGG	GCTCCATTCC	240
ACCGCCTCCC	GCCTCAGCCC	CACCTGTGGG	GCCACATCGC	CACTTCCACG	CCCATGGCCC	300
AGTCCCAGGG	CCCCAACACT	ATACCTTGGG	CCGGCCAGGC	AGGGCACCCA	GACGGGGGGC	360
TGGAGGACAC	CCTCAGTTTG	CTCCACATGG	CCGCCACCCC	CTGCACCAAGC	CCACATCCCC	420
ACTGCCCTCG	TACAGTCCTG	CCCCCAGCA	CCCTCCAGCC	CACAAACAGG	GCCCTAAGCA	480
CTTCATCTTC	AGCCACCACC	CATCTCGAG				509

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTGGCC	TTCATGGCCT	AAAGATGGCC	GAGAACACGG	GTCGGCCCGG	CAAGAGCAGC	60
GGGAGCGCG	CGGGGAAGGG	GGCGGTGTC	GCAGAGCAGG	TGATTGCTGG	CTTCAACCGC	120
CTTGGCGAG	AACAGCGAGG	CCTGGCATCC	AAAGCAGCTG	AGTTGGAGAT	GGAGTTGAAT	180
GAGCACAGCC	TAGTGATCGA	TACACTGAAG	GAGGTAGATG	AAACTCGTAA	GTGCTACCGC	240
ATGGTTGGAG	GAGTGCTGGT	GGAGCGAACT	CTCAAAAGAGG	TGCTGCCCGC	TTTGGAGAAC	300
AACAAGGAGC	AGATACAGAA	GATCATTGAG	ACACTGACAC	AACCAACTCG	AG	352

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTGGCC	AAAGAGGCCT	AGCTAGGTT	TGAAGCTTCT	GAGTTCTGCA	GCCTCACCTC	60
TGAGAAAACC	TCTTTGCCAC	CAATACCATG	AAGCTCTGCG	TGACTGTCCCT	GTCTCTCCTC	120
GTGCTAGTAG	CTGCCCTCTG	CTCTCTAGCA	CTCTCAGCAC	CAATGGGCTC	AGTCCCCCCC	180
CCCGTACACG	CCTCGAGGCA	GGTCGAG				207

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTGGCC	TTCATGGCCT	AGGCAGGGACT	AACACAGGGT	TGTCATCTTT	TCCTTTGCC	60
AAGAAAAGAC	ATTAATATGT	ACTACCAGCA	TCTGCCATCA	CTAGCATTT	ATAAAAAGAG	120
GTTCTGTTAG	CAACAGAGTA	GAAACTGTAG	GAAAGCATCT	CAGAACAAAA	CTAAGTTGAA	180
TAAATTCAAC	TAATAAAAAT	GCCTGGTCT	AGGATTCTT	TTCTTCATCA	AAAGCTGCAA	240
GAGAAAGCCA	CTGCTTACCT	GATGCCGATT	TACTGGTCAT	TGGGGTGGGC	AGGTTGGTT	300
CTCGAG						306

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGTCTCACTT	GTCTCATCCT	GTCGCCAGG	CTGGAATGCA	GTGGTATGAT	CTCAGCTCAC	60
TGCAACCTCA	GCCTCTGGG	TTCAAGTGAT	TATCCCTGCCT	CAGCCCTCAA	GTANCTGGGA	120
CTATAAGCAC	ACATCACCAAC	ACCCAGCCAA	TTTTTTGAA	TTTTTAATAG	GGTTTCACTA	180
TGTTGGCCAG	GCTGGTTGAA	CTCCTATCCT	CAAGCGATCC	ACCCACCTCG	GCCTCCCGAA	240

GTGCTGGAT TACCTGAGCC ACCGTGCCA GCCCATTCA CAGTACTTT TATTTAACCC	300
TATCGTGCTA GGGCACCATG CAATATACAG CTATTCATT TTCTTTTGT CTCTGTTCT	360
TAGGTGGTCT CGAG	374

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAATGGCAG GAATTGCAA TATTGGCATA TGGTTCTTT GGATTAGATT ATATAAAATC	60
AGAAGAGGTA GAACCAGGCC CCAAGCACTC CTTTTCTCT GCATGATACT TCTGCTTATT	120
GTCCTTCACA CTAGCTACAT GATTTATAGT CTTGCTCCCC AATATGTTAT GTATGGAAGC	180
CAAATTACT TAATAGAGAC TAATATAACT TCTGATAATC ATAAAGGCAA TTCAACCCCT	240
TCTGTGCCA AGAGATGTGA TGCAGAAGCT CCTGAAGATC AGTGTACTGT TACCCGGACG	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GGTAGAGATA ACAAAACAGG ATACCAAAGT TGAGCTGGAG ACTTACAAGC AACTCGGCA	60
AGGCTCTGGAT GAAATGTACA GTGATGTGTG GAAGCAGCTA AAAGAGGAGA AGAAAGTCGG	120
GTTGGAACCTG GAAAAAGAAC TGGAGTTACA AATTGGAATG AAAACCGAAA TGAAATTGCG	180
AATGAAGTTA CTGGAAAAGG ACACCCACGA GAAGCAGGAC ACACTAGTTG CCCTCCGCCA	240
GCAGCTGGAA GAAGTCAAAG CGATTAATT ACAGATGTTT CACAAAGCTC AGAATGCAGA	300
GAGCAGTTG CAGCAGAAGA ATGAAGCCAT CACGCTCGAG	340

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAATTCCGCC AAAGAGGCCT AGATTTAAA TTGTTGAT ACCTGCTGTG TATTCCTTGC	60
ATACCCAGCA CATTGTTGCC CATAATTGTG ACATGTAGTA TGTATTTATT ACAATTATAT	120
GATTAATGAA ATGTATCTA TTTTTTTCAT GTATAGCATG TACAGTCACA CTCGAG	176

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAATTCCGCC	AAAGAGGCCT	ATTCTTTGTC	TTTTGCACAT	GTTCCTTGAG	TCTTAGTATC	60
TGTAACGTGG	CGCTACTCTC	TCTATCATGG	GGGGGCATGT	TTTGACATTA	AATTGACTTT	120
TAAGAAAAAC	ATGTCACTAA	CCTGAAGCTC	AGCCACACAG	TGACTTTAA	GGTTTTATTT	180
AGACTTTACT	GTGTTCTCA	TGAGAGTAGG	TACAGACTGC	ATAAGTTTA	GAATCCAGC	240
ATATGTCTGA	AAAGACGGGA	CTTTCACTGT	GATTTCACC	AGAGAAATTA	TAGCAGAGTG	300
GCTGAGCATG	TGCTCTGAGG	CCAGGCCCCA	GCTCTGCTGC	TGACAGCTG	TGTGGTCCTG	360
GGCAGAGTGG	TCTCCGAGTT	CCAGTCCCTC	CTCTGTAAAA	TGGCCTTACT	CGAG	414

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAATTCCGCC	AAAGAGGCCT	AAACATATAC	CTAGTCTATA	CTCTCTCTTA	TCTCTGAACA	60
CTTTTCATCT	GGAGCTATTAA	ATGCCCTCTA	GCCTTTATTA	TAATTATCAC	ATATAATTAT	120
GCCTTTCTC	CTCAAAATTA	TCTGTTGGAG	TCATCTTATA	GTAGAGTCTT	TACAGAACAC	180
AAAGCATTCA	ATCACTTAT	TTCAGACACCC	AACCTTGTIT	TTGATGAACA	TATGTTAGTC	240
TTAACGCCATC	TAAAGTAATG	CTAATGTGGG	ATCTTATGGA	AGACTACTGG	TAATACAGGA	300
AAAAAAGTGG	CAAAGAAATC	TGACACGTTT	GGCAATTATT	CCTGAGGCTC	TGACCTCTCA	360
ATTGTTGAGT	GTGGGAGGTC	ACAGTAAACA	AACCATATAA	AGATCATGTT	GAAAGTCAAC	420
ATTATTAATA	TACCATACTT	GAAGGATATG	TGGTTATTTGT	CTCACGTGTC	CATGTGAAGA	480
GACCACCGTC	CCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GAATTCCGCC	AAAGAGGCCT	AGTTTTGAT	GAATTGTGT	TATTTACTTA	TAACTAGAGT	60
TTGAATGTTT	ATTGGAAAAA	CTTAATCATG	ATCATCTACT	GGTGGCTCGA	G	111

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GAATTCCGCC	AAAGAGGCCT	ATGCAATTCT	GACCAGGAAG	CTCCTCTTAA	ATTGGAAATT	60
CTTAGAAAGG	TATGGAGCAA	AGGAGATCCC	AGCAAACATT	CCGGCATCTA	CTGCTCTTGG	120
GTTCCTTCTG	TGTGGTTTT	TTTGTGTTG	TTTGTGTTAT	GAGATGGAGT	CTCACTCTGT	180
CGCCCGAGCT	GGAGTGCAGT	GGCGCAATCT	CAGCTCACTG	CAATCTCCAC	CTCCAGAGTT	240
CAAGTGAATA	TCCTGCCTCA	GCCTCTCAAA	CAGCTGGAAT	TACAGGTATA	CACCCACCAC	300
CCGAGCTCGA	G					311

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 597 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GAATTCCGCC	AAAGAGGCCT	AAGTGCAGTG	GTGCGATTAT	AGC1CACTGT	AGCCTCAGAA	60
TCCTGGCTC	AAGCTGTCCT	CCCACTTAGC	CTCCCAAAGT	GCTGGGACTA	CAGGCGTGTG	120
CCACGGGCC	CAGCCATTTC	TCGAATATT	TTCAATCTGC	AGTTGTTGA	ATCCACAGAT	180
GCAGAACCCA	TTCTTAATGG	AGGGCTGACT	ATACCTTCT	GATGACCTAA	ATATTTGTGT	240
CCACTTATGG	GACACTCCCT	TCTTAGTGTC	AAGGTTTGAG	AGAAATTGAG	GGCTGTTGA	300
TGGGCAAAGA	TTTATTTATT	TATTTACTGG	CTTATCTACA	ATTGAGACAG	GGTCTCACTA	360
TGTTTCTCAG	GCTAGTTCTA	ACTCCTGGGC	TGAAGCAGTC	CTCCCATCTC	AGCCTCCCAG	420
AGTGCCTGGG	TTACAGGTGT	GACACCCAT	ACCCGGCAGA	GCAAAGAGTT	AAGAGTACAA	480
GACATTGAT	CATCTTGAGG	AGTATTTACT	TCAGACTGAA	ACACCACATG	AAATTCTAGA	540
GTCCAACAGA	AAGTGTATA	ATTTTTGCT	TTTCCCTTCT	TCGGCTACAT	CCTCGAG	597

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 506 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GAATTCCGCC	AAAGAGGCCT	AATTCTAGAC	ATGCTCAGCT	TTGTTGATAAC	GCGGACTTTG	60
TTGCTGCTTG	CAGTAACCTT	ATGCCCTAGCA	ACATGCCAAT	CTTTACAAGA	GGAAACTGTA	120
AGAAAGGGCC	CAGCCGGAGA	TAGAGGACCA	CGTGGAGAAA	GGGGTCCACC	AGGCCCCCCC	180
GGCAGAGATG	GTGAAGATGG	TCCCCCAGGC	CCTCCCTGGTC	CACCTGGTCC	TCCCTGGCCCC	240
CTGGCTCTGG	TGGGAACCTT	GCTGCTCAGT	ATGATGGAAA	AGGAGTTGGA	CTTGGCCCTG	300
GACCAATGGG	CTTAATGGGA	CCTAGAGGCC	CACCTGGTGC	AGCTGGAGCC	CCAGGCCCTC	360
AAGGTTTCCA	AGGACCTGCT	GGTGAGCCTG	GTGAACCTGG	TCAAACCTGGT	CCTGCAGGTG	420
GTCGTGGTCC	AGCTGGCCCT	CCTGGCAAGG	CTGGTGAAGA	TGGTCACCCCT	GGAAAACCCG	480
GACGACCTGG	TGAGAGAGGC	CTCGAG				506

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAATTCCGCC	AAAGAGGCCT	AGTCTGTGGT	CATTITCAAC	TCTCATTTAT	AGGATTCTAA	60
AAGGGCACTA	CATTACTCCA	CTCCCTTATC	TAAAATAAAT	TTAAAATTCA	TCCGAATTG	120
TCCAGTCCTC	CATCACTGGA	AAATGTACAG	ATTCCCTTCTC	TGAAATATC	TAAAGAAAAG	180
TACAGCTAAT	TTTCCCCCAT	TTCGTGTTGT	TTTGTGCTG	CTTTAACTAT	GAACTCATCT	240
GGCCGGCGCG	AGTGACCAAG	CCGCGGGGAG	CTGGGGAGAG	ACGCACCGGG	GCGGGACTG	300
GGCCAGGAGA	CCAGAACACT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GAATTCCGCC	AAAGAGGCCT	AGGAGCAGAT	TCCTCATGGT	GCTTGTATAT	TATATATATT	60
TAATCCGCT	TGACACTTAA	CCCAAGGGAG	ATGGTCCCTT	TTATCAGTTG	AATGTTAGCA	120
GCGTTATTC	AGAGTGTGCT	GACTGGTTAG	AGAAACTCAT	GTACTCAACC	AGCCACAGTT	180
TCAAACAAAA	TTTTTATGTG	CAAAGGACAG	CAACCTCTT	GTATGTTAAA	CCACCAAGTAC	240
TCGAG						245

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GAATTCCGCC	AAAGAGGCCT	AGGTGCTTGT	TTTTAGTCAT	CCCCATGAGA	60	
ATAATAAACT	CCATGAGGGC	AGCAACTTGG	CTGGCTGTG	TGCCAGTGCT	GGGGACATCA	120
CTGAGAAATG	AAGGCCATT	TGGCAGGCTA	TTTTTGAGCA	AGATTCTGA	GGCCCAATCG	180
TTGGGTGATG	AGATGGACCC	GAGGTATTTC	ACTCCAGCTC	TCGAG		225

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GCCAAAGAGG CCTAGAGAGC TCTGGGGGC AACCTGGAGG TCTGAAAAGA GGAGCCAGAG	60
AAGGTGGTAC CAGGCTTCTT GGTCAAGAACCC GGCCTGGAGC TCCTTCCCTT CCCCCTGGCC	120
TGAGAGGTTG CTTTAAGTC TTCCACCCCT TGTTCCATCT GCCTGCCAAC CCATCGGAAA	180
GGAATCCACA TCATATTGGA GATGACCCCA TCAACCCAG GGCTCCAGCA CTACCAAGTT	240
CGAATCCAC GCCCCGGAGT GGGGTAGAGG AAGACGAGAC AGGACGAGGC AGAAAAGCAC	300
ATTTTAAAAA CCAGACAAGA TGGCTAGGCC ATCACCAACC AACGGACTTA CCTTACATTT	360
TTGTAGGTAA TTCCCCCCAA ATCTTGATTT TTTTTTCTT CAATTATCCT TTAAAAAAATA	420
AGAAAACACA TTCCAAACCC ACTCGAG	447

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCGATTGAAT TCTAGACCAT GCCTGCTCTG GGCCCAGCTC TTCTCCAGGC TCTCTGGGCC	60
GGGTGGGTCC TCACCCCTCCA GCCCCCTTCCA CCAACTGCAT TCACTCCCAA TGGCACGTAT	120
CTGCAGCACC TGGCAAGGGA CCCCCACCTCA GGCACCCCTCT ACCTGGGGGC TACCAACTTC	180
CTGTTCCAGC TGAGCCCTGG GCTGCAGCTG GAGGCCACAG TGTCCACCGG CCCTGTGCTA	240
GACAGCAGGG ACTGCCTGCC ACCTGTGATG CCTGATGAGT GCCCCCAGGC CCAGCCTACC	300
AACAACCCGA ATCAGCTGCT CCTGGTGAGC CCAGGGGCC TGTTGGTATG CGGGAGCGTG	360
CACCAAGGGGG TCTGTGAACA GCGGCGCCTG GGGCAGCTG AG	402

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GAATTGGGCC AAAGAGGCCT AGTGGAAAGAT TTGGGTACTG TCTTTAATAA ATCAATCAAT	60
CGACTCTTAT TTCAAGGAGA AAGTTCTATG TTATATGTTG AAGGTGAACA GATCATATTT	120
AGAGGATATA ACAATTAGAA ATCTAGAAA TAATTATCAC TTTTATAAAA TTTTTAGTC	180
ACTGTACAAA TAATTACATA AAACATCAAT TAATTATGCT TAAAAATCAC TAATGTTCAT	240
AATATATAAT CACTATTGT AATCAAAAGT TTAATTATGCT GCCAAAAAAT AAAAAATGCT	300
TACTCGA	307

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAATTCCGCC	AAAGAGGCCT	ACCTCCATAA	CCGTGCTTT	GACGTTAAAA	ATTTTAAATT	60
CAGCCTTTTG	GAGAACACTA	AGTATCTTAG	TGTGTTTTA	CTTACTATAA	TAATATTATT	120
GACCTAGTGT	AATATTACTG	CCATATGGAC	CTCAAGGGTA	CTTTCTGAT	AAATTTCTGT	180
TATGGTTTCA	TAATTTAAACA	AAAGGATAAT	ATACAGAGTT	GTTGGAGTTT	TTTGGTTTG	240
TTTTGGTTTG	AGATAGGCCTG	GGCAACGAGT	GAAACTCTGT	CACACACACA	CACACACACA	300
	CACAGACACA	CACCAAATCT	CGAG			324

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GAATTCCGGCT	TCATGGCCTA	CAAGAAGATG	AAGAAGATTG	TGGATGCCGT	GATCAAGTAC	60
AAGGACAGCA	GTGGACGTCA	GCTCAGCGAG	GTCTTCATCC	AGCTGCCCTC	GCGAAAGGAG	120
CTGCCCGAGT	ACTACGAGCT	CATCCGCAAG	CCCGTGGACT	TCAAGAAGAT	AAAGGAGCGC	180
ATTCGCAACC	ACAAGTACCG	CAGCCTCAAC	GACCTAGAGA	AGGACGTCAT	GCTCCTGTGC	240
CAGAACGCAC	AGACCTTCAA	CCTGGAGGGC	TCCCTGATCT	ATGAAGACTC	CATCGTCTTG	300
CAGTCGGTCT	TCACCAGCGT	GGGGCAGAAA	ATCGAGAAGG	AGGATGACAG	TGAAGGCGAG	360
GAGAGTGAGG	AGGAGGAAGA	GGGGCAGGGAG	GAAGGCTCCG	AATCCGAATC	TCGGTCCAGT	420
CTCGAG						426

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GAATTCCGGCC	TTCATGGCCA	ACACATAATC	CACGCTCATC	TTGCAAAGCG	CTATTTCAGG	60
CACATCATTG	GAATACAGGA	AGTAGCCCTG	CACCTGCCAG	TGAGCTCGCC	ATTCACTGAT	120
TGGAAAGAGTG	ACCTGGCATC	TTGAAATCA	TTGTGTCGCT	TCAGGAGAAAT	GTGCAGTGTC	180
TTGTAACAAC	TAATTATAAT	GCAAATTAGG	GCTACATTGT	AATCTGCTTT	GTAAATGAAA	240
ATGATAAAAC	AGAATATTGA	CAAGCTAGGA	CACCTGTGGT	ATCTTTAATT	GTATCTCCTT	300
CAGAAAGTTG	CTTCTTATGG	TATAATAAG	TATGGAAGAA	TATTGAGTAT	ATGTTTACTC	360
TGGGCCTGGG	AGAACTTAAC	TTTCTAGAGC	AGTTTGTGTA	CTTGTGTGCA	ATGGGGAGAG	420
GTACCATGAT	GACACTCACA	GGGAGCCACT	GTTCACTGAC	ACTTGGAAAGG	CCCTGCCTCG	480
AG						482

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GTGTTGCC	ACACCCTCCT	TGAATTAAC	TGCCACAATC	TATCCGCAGA	TGTGTTTGT	60
TCTGTTCTT	GTTTTCACT	ACCGTTGCG	TGCTTCCTC	TGAAGCCAGA	GGGTGAAAGG	120
CCCTAGAAA	GTTAGITATC	AGTCAACTGA	TGATAACTGT	GATCCTTAA	GATGAATTCC	180
CAGCCTGAGG	TGACACACAG	AGGTTCAGCA	GACGTCTAG	GATCTGTCAC	ATGTCATGTT	240
GCTTGGTGTG	AAGATGGAAG	AACAAAGTC	ACATCAGTT	CTGCTCCTTC	AAACAGTGTG	300
TCGATATGAA	ACATTGAGAT	TTGGCAGAAA	CATGTGCC	GTTTSCAGCA	CCAAATACTC	360
GAG						363

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GAATTCCGCC	TTCATGGCCT	AAAGGGATAT	TCACTCAAAT	CCCTAAGTAT	TTCAAGAAACA	60
GCCTGAGAGC	AAGTCCTTG	CTTCGCTTTC	TAGTTTAAA	AGGCTTTAA	CTGTTTAGTC	120
TGAGATTCCC	CTAAAAGTC	CAGGAAAGCA	AACTCAAAAA	GAGCCTAGGT	GGTCAATCAT	180
TATTTTGCT	GCGTTTATAT	AAATAATCA	CCAAAGTTAA	TGAGACTAAA	CTTATTTGCA	240
AAGCAAATCA	GTCTTGCTT	ATTTTGCTA	GGAAATGGGG	TAAATGGAGA	GAGAGAAATT	300
ATGTTTCAGA	AGAAAACAT	AGCACACCAA	CTCGAG			336

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAATTCCGCC	TTCATGGCCT	AGTGGGAAAC	ATTATTCAA	GACATTAGGG	ATAAGAATGC	60
CAGTTGCTAC	TGAGTTGGTT	ATTGTTCAA	GGATTTATCA	ATACATAGAG	CAAATAATTA	120
TGTTTGCTT	TGTCTTATTT	TTATTTCTTT	ACTTTAGAAA	CAGTACAGCT	ACTTACAAT	180
CAAGTTTACA	ACTCTCAGGT	TATCTAAAT	CTGAAGCTTC	TACCTCCTA	AGAACAAAAC	240
ACCGGCTCGA	G					251

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTTCAAACCA	TTCAAATACT	TTTCAACCT	CTATTTCTTA	CTTCTTGCT	GCTCTCAGTT	60
TGTTCCGAA	ATGAGACTTG	GTGCACTCTA	TACCTACTGG	GTTCCCTG	GCTTCGTGCT	120
GGCCGTCACT	GTCATCCGTG	AGGCGGTGGA	GGAGATCCGA	TGCTACGTGC	GGGACAAGGA	180
AGTCAACTCC	CAGGTCTACA	GCCGGCTCAC	AGCACGAGGC	ACAGTGAAGG	TGAAGAGTTC	240
TAACATCCAA	GTGGAGGCC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 437 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GAATTGGCC	TTCATGGCCT	AAGATGATTG	TGCTATTATT	GTTTGCCTT	CTCTGGATGG	60
TGGAAGGAGT	CTTTTCCAG	CTTCACTACA	CGGTACAGGA	GGAGCAGGAA	CATGGCACTT	120
TCGTGGGAA	TATCGCTGAA	GATCTGGTC	TGGACATTAC	AAAACTTTCG	GCTCGCGGGT	180
TTCAGACGGT	GCCCAACTCA	AGGACCCCTT	ACTTAGACCT	CAACCTGGAG	ACAGGGGTGC	240
TGTACGTGAA	CGAGAAAATA	GACCGCGAAC	AAATCTGCAA	ACAGAGCCCC	TCCTGTGTCC	300
TGCACCTGGA	GGTCTTCTG	GAGAACCCCC	TGGAGCTGTT	CCAGGTGGAG	ATCGAGGTGC	360
TGGACATTA	TGACAAACCCC	CCCTCTTCTC	CGGAGCCAGA	CCTGACGGTG	GAAATCTCTG	420
AGGGGCCAC	ACTCGAG					437

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAATTGGCC	TTCATGGCCT	AGTACCTTAA	AAACTTTGGA	ATAATAATA	ATAATAATAA	60
ACAAAAAAATA	ATCCCAAACC	CCGTAAGTTT	AACTTTCTAT	GCTTGGCTG	TTTTGGTTT	120
ATTTTTGTT	TTT TAGAAGG	GGTCTCGCTC	TGTCGCCAG	ATGGAGTG	AGTGGCTTAA	180
TCAGGGCTCA	TTGCAGCCTC	GACCTCCTT	GTCGGGCGA	TCCTCCTCCC	TCCACACTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AATTAAATTA	AATTAAAATC	TTTGTACAA	ACTATGAAAA	TGAATATAAG	TAAATTTCAT	60
ATCATTCTT	TTCTAGATT	ATTATCTAGG	ATAGATTGG	ATGAACATAAT	GAAAAAAAGAT	120
GAACCGCCTC	TTGATTTCC	TGATACCTCTG	GAAGGATTG	AATATGCTTT	TAATGAAAAG	180
GGACAGTTAA	GACACATAAA	AACTGGGGAA	CCATTTGTTT	TTAACTACCG	GGAAGATTTA	240
CACAGATGGA	ACCAGAAGCT	CGAG				264

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GAATTCCGGCC	TTCATGGCCT	AACTTGGAGA	AACTATTAA	GTGGATGAA	GCAAGTGCCC	60
AGCTCCTTGC	TTATAAGGAA	AAAGGCCATT	CTCAGAGTTC	ACAATTTC	TCTGATCAAG	120
AAATAGCTCA	TCTGCTGCCT	GAAAATGTGA	GTGCGCTCCC	AGCTACGGTG	GCAGTTGCTT	180
CTCCACATAC	CACCTCGGCT	ACTCCAAAGC	CCGCCACCC	TCTACCCACC	AATGCTTCAG	240
TGACACCTTC	TGGGACTTCC	CAGCCACAGC	TGGCCACCC	AGCTCCACCT	GTAACCACTG	300
TCACCTCTCA	GCCTCCCACG	ACCCCTATT	CTACAGTTT	TACACGGGCT	GCGGCTACAC	360
TCCAAGCAAT	GGCTACAACA	GCAGTTCTGA	CTACCACCTT	TCAGGCACCA	TAGTGACTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAATTCCGGCC	TTCATGGCCT	ACCGAAGGGC	ATCCCATCGG	TTGGGTAGGT	CATGGTTAAA	60
AAATCATCTC	CTTGGGTGTC	ATATTTAATT	ATTTTCCACT	ATTTTTCCCT	CACACAAAAT	120
GATTTGGCCC	GGTACCCCTT	TTGGGGGTGTC	ACAGTCCATG	AGATGAATAT	TGAATGGGGA	180
GACCTGGGTT	CTAGTCTCGC	ATTTACCACT	CAGGTTACAA	TGCGACCTTG	AGCAAGTCAC	240
TTCACCTCCC	AGCGCCTCAG	TTTCCTCATT	GTAAGATAGG	AAAAGCCTTG	TCATTTTAA	300
AATTTTATTT	TTTGCATATA	CCTCATGGCG	AACTCGAG			338

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GAATTCTGGCC	TTCATGGCCT	ACTATGCTCT	GCACGTGGGT	CATTCTTAC	TGGTTTCTAA	60
AAGCCTTTCA	TTTTCTGCCT	GTACACAATA	GCCCCCTTCC	TCCATTGTTT	TTAGGATCCT	120
TTTTCTCTT	ACCAAGCTGT	AACCTGGAAG	TATTCTTCT	TCATCCCAGA	TCTCCCAGT	180
CCTCCCCACT	TCTATTGTT	TCCATCCAAT	GTGGATTCA	GATCATTTA	TGGATTAA	240
ACTACTCTGG	GGCTACCCCTC	GAG				263

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAATTCTGGCC	TTCATGGCCT	AGAAACACAT	GTGATCTGTA	CTCATGAGAA	CCTGTAGTTA	60
ACTATACGAG	CCTTGCTGTG	CATTTGTTT	TTATCTGAGC	CTGTCCTTCA	ATGTCCTATC	120
CCTTGAGAGA	ACTGAGGGCT	GAGAACCAAG	CTTTCCGAAG	CGGTCTGAGT	GTCAGCGGTG	180
GTAGTGGTCT	CTGGAGAAAA	GAATCGAGAC	AGGATAGGAC	TTGGAGAAGA	GTGAGTCATT	240
GTTACCCAGA	AACCCCTGGAG	AAACACTGGAC	TCGAG			275

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGGCGTTCTC	ACGCCCGCAA	CAATTCTGA	GTAGGGCCTT	GCTTGAGTTC	TTCGGAAAGT	60
CTCATCCACC	CCCACATCGC	CTCTTTAGGA	AGTCATTAA	TGTTGGCCTT	CATTATTCCC	120
ACATCCCTTT	CCTTACTACT	TGCCTGACT	TCTTGAGAAA	AAGACTGCAG	AAAGGAGAGG	180
TGGGGCTTC	AGTAGAAACA	AGCAAACCGC	AGGTCCCTGT	GGGGGGACTC	TCCAGGAAGA	240
AGGGTAATTT	CCTGCTCCT	TAAATGGCT	GCTACTGTCA	GTTATTTGTC	TCCCAACCCCC	300
AGAGCTTCAC	TTGCTCCCTC	ACTTCCCAGT	TCCGCAAGAA	CCGTGGGCGA	CAGTTATGGA	360
GAAGCGCTG	CAGGAGGCTC	AGCTGTACAA	GGAGGAAGG	AACCAGCGCT	ACCGGGAAGG	420
GAAGTACCGA	GATGCTGTGA	GTAGGTACCA	TCGAGCTCTG	CTTCAGCTGC	GGGGTCTGGA	480
TCCGAGCTG	CCCTCTCCGT	TACCTAATCT	CGGACCTCGA	GGCCCGGCC	TCACGCCCTGA	540
ACGACCTGCC	TCGAG					555

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTGAAGATGG	ACTGCTCTGG	GGCCCATGTG	CAAGTGACCT	GTGCCAAGCT	CATCTCCAGG	60
ACAGGCCACC	TGATGAAGCT	TCTCAGTGGG	CAGCAGGAAG	TAAAGGCATC	CAAGATAGAA	120
TGGGATACGG	ACCAATGCAA	GATTGAGAAC	TACATTAATG	AGAGCACAGA	AGCCAGAGT	180
GAACAGAAAAG	AGAAGTCGCT	TGAGCTCAA	AAAGAAGTTC	CAGGATATGG	CTATACTGAC	240
AAACTCATCT	TGGCATTAAAT	TGTTACTGGA	ATACTAACGA	TTTGATTAT	ACTTTCTGC	300
CTCATTTGTGA	TATGTTGTCA	CCGAAGGTCA	TTACAAGAAG	ATGAAGAAGG	ATCACTCGAG	360

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GAATTCCGGCC	TTCATGGCCT	AGCTCCTGCG	TAAAGGAGCA	TGAGAGCGTG	GGAGTTTTC	60
AGTGGCCGTG	GGGTTCTTCG	TCCGCTCTCG	GTCCGGCGTC	GCTTTCTGCA	GCTCCGTCA	120
GGGAGCGCGA	GGCCTGTTAT	TAACCGCGGA	GCGCTTGTGTC	ACGAANTCCC	TGTGGCGTCT	180
TGAAGAAGGC	ATCCCCCACC	CGCCAAATGG	CgtccatGCC	CCCGACGCC	GAGGCCAGG	240
AGACTCGAGG	TACCTTTTTC	GTCCAAGTTT	ATNGCTGCTT	TGGTCTCTG	CCTGACCCCN	300
TCCTTGGAG	GAGAGTTGGG	CATGCCCTGTT	GTGCTAGGAG	TGCTCNTGAG	CCCCAAATAG	360
CCCTTGACCC	AAAGTGTCTT	CGTTCCAAGA	CCACACACAT	AATGGTTTAC	CAACTTCNTT	420
CTTTCAGAAC	TACCAACTGG	GAGCAAGGAC	CTGTGGAGGA	ATCTCTGAGA	GAGTTTCTCA	480
ATGCTTTATC	TGTTTGTGTTT	GTGCTTGTG	GAGATAGGGT	CTGGCCCTGT	CGCTGGAGTG	540
TTGCTTGCT	GGCTGGAGTG	CAGTGTGAT	ATCATAGCTC	CgtctggAAC	TCAGGAAATC	600
CTTAACGCCCTC	AGCCTCTCGA	G				621

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAATTCCGGCC	TTCATGGCCT	ACAATTGGG	GCAAGGCTTA	GCAGAACACG	GCGGCATGAG	60
CAGCGTGACT	CAGGAGGGCA	GACAAGCCTC	TATCCGGCTG	TGGAGGTAC	GTCTGGCCG	120
GGTGATGTAC	TCCATGGCAA	ACTGTCTGCT	CCTGATGAAG	GATTATGTGC	TGGCCGTGGA	180
GGCGTATCAT	TCGGTTATCA	AGTATTACCC	AGAGCAAGG	CCCCAGCTGC	TCAGCGGCAT	240
CGGCGGATT	TCCCTGCAGA	TTGGAGACAT	AAAAACAGCT	GAAAAGTATT	TTCAAGACGT	300
TGAGAAAGTA	ACACAGAAAT	TAGACGGACC	TCTCGAG			337

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GAATTCTGGCC	AAAGAGGCCT	ACATTACTGG	GTTAGAAAAC	AAAGAGGGAG	TGCCCTGCAC	60
ATTTCTTTT	GTCTTTAA	ATGTTCTTA	AGTTGGAACA	GGTTTCCTCG	GGCCTGTTT	120
GAATGATTGC	TGGAGTGCAT	TTGATAGTTA	AAAATTACTA	ATTGGTTTA	TTTCCCTTCA	180
CACTCTGCCT	CCCTTATTTC	CCCCAATTGA	CCCTAAACCT	CGAG		224

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GATTTAATGC	ATGCTAGCAA	CAGCTTAAC	TTTGGATTCA	GTTATTTGAA	ACACTTTCC	60
GGCATCTTC	CCTTTCTAAT	GTTGTGGGGT	GGAAACCGGA	TGGCAAATCA	CTGTGAGCGG	120
GATACCTCA	CACAGTCCAC	CTTGTGTGTG	ACTTCACAAA	TGGGGACTT	CACAAATGGG	180
GTAACGTAA	GTTATTACTT	TCAAATTTG	ACATGGAGCA	TTATGATCAA	GGAAATGGG	240
CAACTCGAG						249

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GCTGCGCCGC	ACCCCTGAGAG	ATGGTTGGTG	CCATGTGAA	GGTGATTGTT	TCGCTGGTCC	60
TGTTGATGCC	TGGCCCTGT	GATGGGCTGT	TTCACTCCCT	ATACAGAAAGT	GTTTCCATGC	120
CACCTAAGGG	AGACTCAGGA	CAGCCATTAT	TTCTCACCCCC	TTACATTGAA	GCTGGGAAGA	180
TCCAAAAGG	AAGAGAATTG	AGTTTGGTGG	GTCCTTCCC	AGGACTGAAC	ATGAAGAGTT	240
ATGCCGGCTA	CCTCGAG					257

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAATTCTAGA CTTTGTCTCC AGAGCATTGC CTTTATAAGC AGATTGGCAC CAACAGTTCC	60
ATAGTTAAC ATCTAGTTAA GCTACAAATA TAGTATAAGC ATTATTAGCA GCTGGTACTT	120
CTGCTAGGGG TTGTAATTC CAGGTGTTAC ACTGACCTCA ATCCAATTAA CATAATTAC	180
ATAAAATGCAT CTCGGTGGAA AAATAATCAT TTTCTTGCA TATCTCGAG	229

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

GAATTCCGCC TTCATGGCCT ACACGTGCTAT GTATGTTTC TCCTTAATGA TGAAGAGTGT	60
AGATGATGCT AATAATAGTA GCTGATGTAC TGACTTTAG CTGTCGCAA AGCCATGTC	120
AAAATACCTT ACAAGTGTAA ACTTGTGTTA TCTTCACAAAC AACCTTAAGA AGTGGATATT	180
ATTAAGTAG ATTTTGAAG ACTGATCTAT TTAATTATTA ATAGATCTGT CTCATTCCCTT	240
TTTCCCCCA ACTCGAG	257

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 223 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

GAATTCCGCC TTCATGGCCT ACGCGTCTGC TTGGAGACCC GTAAGGATAT TGATGACCAT	60
GAGATCCCTG CTCAGAACCC CCTTCCTGTG TGGCTGCTC TGGGCTTTT GTGCCCGAGG	120
CGCCAGGGCC TTTGTGCC CAGGCCAGG GGCTGAGGAG CCTGCAGCCA GCTTCTCCCA	180
ACCCGGCAGC ATGGGCTGG ATAAGAACAC AGTATCACTC GAG	223

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GAATTCTAGA CCTGCATGTC CCAGTGTGAA ATTCAGCAC GGCATTTCT GCATCCTTTC	60
ATGCCCATCC AAAGGATTCC GCTGCAGAAA TTATTGATGT GCTATTTTG CTGTCCTGTG	120
ATGCAGGCTG CTTGGGCCCT CTGGGTCACT CTTCCAAGGC TGCAACTCGA G	171

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GAATTCCGCC	TTCATGGCCT	AAAAAGAAA	AGAAAAGTAA	AAGGAAGAAA	CAAGAACAAAG	60
AAAAAAAGATT	ATATTGATT	TAAAATCATG	CAAAAACCTGC	AACTCTGTGT	TTATATTTAC	120
CTGTTTATGC	TGATTGTTGC	TGGTCCAGTG	GATCTAAATG	AGAACAGTGA	GCAAAAAAGAA	180
AATGTGGAAA	AAGAGGGGCT	GTGTAATGCA	TGTACTTGG	GACAAAACAC	TAATCTTCA	240
AGAATAGAAG	CCATTAAGAT	ACAATCCTC	AGTAAACTTC	GTCTGGAAAC	AGCTCCTAAC	300
ATCAGCAAAG	ATGTTATAAG	ACAACCTTTA	CTCGAG			336

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

GAATTCCGCC	AAAGAGGCCT	AGAAGAGCAA	GCGCCATGTT	GAAGCCATCA	TTACCATTCA	60
CATCCCTCTT	ATTCTGCAG	CTGCCCTGC	TGGGAGTGG	GCTGAACACG	ACAATTCTGA	120
CGCCCAATGG	GAATGAAGAC	ACCAACAGCTG	ATTTCTTCT	GACCACTATG	CCCACGTGACT	180
CCCTCAGTGT	TTCCACTCTG	CACGCTCTCG	AG			212

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GAATTCCGCC	TTCATGGTCT	ATGCTACTCA	GTTGGATCTA	GCAGAAACAA	AAGCTGAGTC	60
TGAGCAGTTG	GGCGGAGGCC	TTCTGGAAGA	ACAGTATTTT	GAATTGACGC	AAGAAAGCAA	120
GAAAGCTGCT	TCAAGAAATA	GACAAGAGAT	TACAGATAAA	GATCACACTG	TTAGTCGGCT	180
TGAAGAAGCA	AACAGCATGC	TAACCAAAGA	TATTGAAATA	TTAAGAAGAG	AGAATGAAGA	240
GCTAACAGAG	AAAATGAAGA	AGGCAGAGGA	AGAATATAAA	CTGGAGAAGG	AGGAGGAGAT	300
CAGTAATCTT	AAAGGCTGCCT	TTGAAAAGAA	TATCAACACT	AAACTCGAG		349

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGGGGCTAGT	CATGGCGTCC	CCGTCTCGGA	GACTGCGAC	AAACCAAGTC	ATTACTTGT	60
TCAAGAGCGT	TCTGCTAATC	TACACTTTA	TTTCTGGATC	ACTGGCGTTA	TCCTTCTTGC	120
AGTTGGCATT	TGGGGCAAGG	TGAGCCTGGA	GAATTACTT	TCTCTTTAA	ATGAGAAGGC	180
CACCAATGTC	CCCTTCGTGC	TCATTGCTAC	TGGTACCGTC	ATTATTCTTT	TGGGCACCTT	240
TGGTTGTTTT	GCTACCTGCC	GAGCTTCTGC	ATGGATGCTA	AAACTGTATG	CAATGTTTCT	300
GACTCTCGTT	TTTTGGTCG	AACTGGTCGC	TGCCATCGTA	GGATTGTTT	TCAGACATGA	360
GATTAAGAAC	ACCTTTAAGA	ATAATCTCGA	G			391

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GAATTCGGCC	TTCATGGCCT	AGGGAGTCTG	AAGCAATTTC	TGAAGAAGAC	CAAAAAGAAC	60
CACAAGACGA	TGAATGAAAA	GGCATGGAAG	CGTTGGTGC	CACAAATCCT	CTCTGCCCTA	120
AGCTACCTGC	ACTCTGTGA	CCCCCCCAC	ATCCATGGGA	ACCTGACCTG	TGACACCAC	180
TTCATCCAGC	ACAAACGACT	CATCAAGATT	GGCTCTGTGG	CTCCGTACAC	TATCAACAAT	240
CATGTGAAGA	CTTGTGAGA	AGAGCAGAAAG	AATCTACACT	TCTTTCGACC	AGAGTATGGA	300
GAAGTCACTA	ATGTGACAAC	ACGAGTGGAC	ATCTACTCCT	TTGGCATGTG	TGCACTGGAG	360
ATGGCAGTGC	TGGAGATTCA	GGGCAATGGA	GAGTCCTCAT	ATGTGCCACA	GGAAAGCCATC	420
AGCAGTGCCA	TCCAGCTTCT	AGAAGACCCA	TTACAGAGGG	AGTTCAATTCA	AAAGTGCTG	480
C						481

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATTCGGCC	AAAGAGGCCT	ACGATTGAAT	TCTAGATCTG	CCCGTCTTGG	CCTCGCAAAG	60
TGCTGGGATT	ACAGGGCGTGA	ACCACTGTGC	CTGGCATATT	TGTCTATTAA	TTTGTCTTTTC	120
TTTGTGATGA	TTCTAGAGGG	GGGAAATCA	GTAGAAGAAC	AGTTATGTA	TCTTAACAAG	180
TTCTCCATGT	GTCTTGCCAT	CTNGCTTTTT	CTCATCCTAT	CAGTACTGGA	TGAGAATGTT	240
TATTTCACTG	AACTTTGCCA	AAGAGTTTCA	ACATTTTTT	GTTTAATCAT	AGGAGAAAAAA	300
GGTTTATCTT	ATTTTTAAAA	ATTTTTATTT	AATTCTTCA	TTACAAATGA	AGTCCCAGAA	360
GTGTGATTTG	TTTCTTTAGG	CTGTTCTTAA	TTGTTCATG	GAACAGGCAG	GGTTGAAGG	420
AGTGGGGATA	CTGGGAAAGC	CAGGGTGTATG	AGAAAATAGG	AAAGGGGTCT	TGTCATTGGG	480
AGGCCACTAT	ACCACTGCC	CTTGTACCAAG	GACTAATATG	GTACTTTGAA	GCTTTAAATT	540
CATTTCTTAA	TTCAATAATT	TTAGGCATCC	CAGGATACTC	GAG		583

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GAATTCTGGCC	AAAGAGGCCT	AGCTATCCGC	TTTGCTATT	TAGTGGCATT	ATCAAAATCA	60
CTGGAAGCAC	CTGTNGTAAT	ATGGTCGGTT	CCAAATATAA	GCTCCCTGTC	CACTCTTCCT	120
CCCATACTAA	CATCCATTG	TGCAAGCAGC	TGGGCTCTAG	TTTCATTCCA	TCTGTCATT	180
TCAGGTAACA	GGGACACATG	TCCAAGTGT	GGCCCCGTG	GCATGATTGT	AGCTTTGTTG	240
ATAGGCATTC	CATCTTTGT	GTAATATGCA	ATAATGGCAT	GACCAGATT	ATGATATGCT	300
GTGATGGTT	TGTGTTGTT	ATCAATTCTC	ACACTTCTC	TTTCAGGCC	CATTAGAATT	360
TTGTCTTGG	AAAACCTCCAG	CTCCTTCATG	GTAACCATT	CTTTCCATC	AACAGCTGCT	420
TTTAATGCAG	CCTGGTTCAC	AAGATTCTCC	AACTCTGCTC	CGGAAAAGCC	AACAGTACCT	480
					CGAG	484

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

GAATTCTGGCC	AAAGAGCCTA	ATTGAAATTCT	AGACCGCCT	CATCGTTCTT	TGCCCTCCTG	60
GTCACCATCT	GCTACGCTGG	AAATACATAT	TTCAGTTTA	TAGCATGGAG	ATCCAGGACC	120
ATACAGTGT	TTACCATTT	GATAATTTAA	AGGAAAAAAA	AAGGAAGACT	CTCACTGTAA	180
AAACAGCTGT	AGGTATAATG	TATAATTCCA	GAGAATTGTA	TTTAACATAAT	TAATGTTTTT	240
TATATTCTTA	AATTGCTCA	CAAATTGTTG	TTTGTACAA	TTAAACTGGA	TACTTATTG	300
CAAAGTGTG	TAGCTTATAA	TGAACCTTTA	AGTATCTTAT	TAATGTATTA	ATGTCTTCAT	360
AGATCATATT	TTCTTAGACA	ATGTTAAAT	AGATAAATTG	CTAATATTGA	GAATGTGTCA	420
					AGTTGTAAA	458
					CCTAACCTTT	
					AAGATGCCAG	
					AACTCGAG	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GAATTCTGGCC	AAAGAGGCCT	ACGGCCAAG	AGGCCTAGGT	GGTGATTGAC	CTAAGAAAAA	60
AGTGTCTTAA	ATATCTGGAT	TCTATGGGAC	AAAAGGGCCA	CAGGATCTGT	GAGATTCTCC	120
TTCAGTATT	ACAGGATGAA	AGTAAGAAC	GCTCGAG			157

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

GAATTCGGCC	AAAGAGGCCT	AGTGGACTGC	TACTTCCCTT	TAGCACTATA	TACAAACATA	60
ACTGCTACTT	CCCTTTAGCC	CAGGATCAA	ATAATGATT	AGTTAAAAGT	TGCTTGCCTA	120
ACAAAATTC	AAAATATGGA	CTTCCTGAA	TTGCTAAAAC	ACATCCTTT	AACTAGGCAT	180
CCTTAAGTCT	ATAGTATCTT	TAAAGTTAAT	TTCAAAATTT	AGCAGAGCCT	GGAACACAAA	240
TTATTTCAGGA	AATAATTCTC	GAACCTACCT	CTATCTTCAT	AAAACGTATT	GGGGCAAGAA	300
CTATTCTATT	GAATTCTAGA	CCTGACTCGA	G			331

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GAATTCGGCC	AAAGAGGCCT	ACCATCTGTC	ACTAATATCA	AAGGAGGGCC	AAGGACACAG	60
CCCTGGGGGA	ACTTACCAAGG	TCAACCCACA	ATGGGTGAAT	TTATAGTTTG	TTAGTTAGTG	120
GTCAGTTACC	AACTTCTCTG	TCTGTCTAAT	GCTTGTACTA	AAATGTCCAG	ATTATTTACC	180
TAGTTAACAA	AATTAAAGAA	GATTCTAAGA	CCAGTTTACG	ATCATTTTCT	CTGAAGTCCA	240
TAATGAATGT	CTGTTAAACT	CTCGTCACTC	TTATTAGGT	GCTTTGGGT	CATTTGTTGT	300
AGGTTCCATTC	TCCCCTAACATCA	ATGTCACATA	TACGCTCTGA	ACTTGTGTTA	TCAGCTTCCT	360
TCCTAGGGCT	TTAACCTCTT	TTCAGTCTTA	TAGCATTCCCT	TCCATTTCC	TTTCAGTTCA	420
CTCCAAATAAA	AGCTCGACAA	ACTCCTGGGA	GCCCCTTGGT	GCTCGAG		467

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

GAATTCGGCC	AAAGAGGCCT	ACGATTGAAG	TCTAGATGCA	CACATTCA	TTCTGTCTCA	60
GTCCTGAGAG	TGGTTGTGTT	TTATGGCTG	ATGAGTTATT	TCCACATATC	ACATGTATAA	120
GGTATTGAA	TGAAGGTGCT	TTGTAGTCAT	GACACACTAC	TCTTTACTA	ATTATTAATA	180
TCTTAAGATT	ACAATTGAG	AGGTAGAGAT	GGTATTGTTT	TTAATGGGTG	TGGGGGGTGG	240
TGATGATAGG	TATTTTAC	CTGGTAAGTG	ACCTACTAGG	TTTTATTAAG	TGTTGCAACT	300
TGTCCAGTGT	GTGGATGGGA	TCTCGAG				327

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

GAATTCGGCC AAAGAGGCCT AGTGGTGGTA TGTATTGAG TTCACAGTAT TTGTTTTATA	60
GCAGTTTGC AAGCACATAC TGTGCCACCG ATTTCACAC ATTATTTTTA GACAAGGGAA	120
CACAGCCATC AAAACTGATA CCATGGCCCG GCGTGGTGGT CGGTGCCTGT AGTCCCAGCT	180
ACTTGGGAAC TCGGGACATT CTCGAG	206

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

GAATTCGGCC AAAGAGGCCT CCACCATGCC CGGCCTCAAC GATATTGATT CTTGGGCTG	60
TAGTCAGTAT TGGATTATGA TCAATATTAT CACCATTTAT TTTGTTGCTC CAGTCTTCC	120
AGCTGTGCC AATCCTTCAG TTGGATTCTT GTGCCCCATC AACATTCTCC ATCCTCTCT	180
CGAG	184

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

GAATTCGGCC AAAGAGGCCG ACTTTATTAT ACCATACATA CTATAGGTAC CTGGGCACAA	60
GATAGGTCAAG GGGGTACTGT ACCCTATTT ACATGCTAA TCACATCATA AGTTTGCAAG	120
TGGTACTTGA AATCATCACT AATGAGACAG CAAATATGTT AGACTTGCTG GCCCAGCAAG	180
CCACAGAAAT AAGGATCACC ATCTATTAGA ATAGACTGGC TTCAAACTCG AG	232

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GAATTCCGCC	AAAGAGCCTA	CTAAAATTCC	TTGTTTGTG	TTTTAATAT	TCCATCGTTG	60
ATAGTTAATA	TTCTTTNGA	GGTTTGTGTT	TAGACAAAGT	AATGTTTTTC	TGAATGATT	120
CTAAGACAAT	TGGTCAGAAA	TAGTCTCTGC	TTGTTGGTT	TATGTTGGT	CAGTTGTGCT	180
TTGATTATAG	ATGGTTCCTC	ATCTGAGATT	AAAGTGGGAC	AGAACTTCAA	AACTAAAAGG	240
GTAAATGTT	GCTGTGATGC	TTATGTGGCA	CATGTGCTAG	TCCCTGATAG	TGGCGAGAAA	300
GATCTTAATT	GCTCAAAGGA	AGTACTCGAG				330

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

GAATTCCGCC	AAAGAGGCCT	ACAGTGCATT	ATGTTATTTT	GTTATCTCTG	CAGTAACCTT	60
CTATCATGTT	ATTATTTTC	TTTGTCTTAT	TTAAAGCTTC	TGAGATTATG	GATTTTGTGTT	120
TCCTTCCCTG	AAAGTTAAGTG	TTATCATTCC	TATATAGTAC	TAAGCTGTCT	ACAGAAATAGT	180
GGGAGTCTGC	CCTCTTGAGT	GGGGAAAGATC	CTAGTTGAA	TCTTCGCTGT	GGGACTTTAA	240
AGTTCAATTAA	CTTCTCTTAG	CCTCAGTCAC	CTGAACCTG	CAGTGGGGAT	CCTTATGCCT	300
CAGAGTGTCA	TTGGGAGGAC	TCACGAAAAT	ACGCTTGAC	TTTGAGTTCA	GTACCTAGCC	360
TGTATGAGCC	AGCATTAAAGA	GGGACAGTC	TCACGCAGCG	CTTTCACAC	AGCTCTCACG	420
CCACATCCTT	TGGCTACTGT	TTTGGTAAAT	CTTTACTAGT	AAATGTTCT	TAAAAGCATT	480
TACATTCA	GACATGATTG	CCTCGAG				507

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

GAATTCCGCC	AAAGAGGCCT	AGATTGAATC	TAACCTTTT	GCCTCTTCCC	AAAGTAGCCTA	60
TTTGAGCTAG	AACAAAACCT	TGTTAGCCAT	TTGGGAGAG	AATAGGGAAT	CTAGAGAATG	120
AAGATCTGCC	CGACCTGCCT	CGAG				144

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

GAATTCCGCC	AAAGAGGCCT	AACGACGGTA	ATCAAGTTT	GCTCCAGAAG	CATCAAGAAA	60
CTTAGCTACT	GCTTCCAAAT	CAGTACCGGT	TTCAGTTAAG	CCTTGAATAA	TACAGTCTTG	120
AAACTGAGTA	GGGTCAAACC	TCTCTTTTTC	ATCTCTTTT	CTAGTTTAA	AACGCTGGCC	180
TGATAGCGTT	GGCTTTGCT	GCTTTTGATT	ATTCAAAAA	GACACCCGAA	TTTAAGGCAG	240
AGAGGAAAGA	GCCAGAAATC	CCCGATGTAC	CGGCAACTGC	GGCGCTATCT	CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

GAATTCCGCC	AAAGAGGCCT	AGACTGCTGG	TGGTGAACCTG	CTTTCTTGT	AGGTTGTGAG	60
GGCTGAAAAAA	GCCAACTTAA	ATAGACATGA	GGCTCATGTT	TGACACAGTGT	GCTCTCGAG	119

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

GAATTCCGCC	AAAGAGGCCT	ACTCAGCTGC	AAAAAAAGCAT	ATTTCTGTG	TTTCTGGACT	60
GCACGTGNGT	CCTTGCCTCT	ACATAGACAC	TCAGACACCC	TCACAAACAC	AGTAGTCTAT	120
AGTTAGGATT	AAAATAGGAT	CTGAACATTC	AAAAGAAAGC	TTTGGAAAAA	AAGAGCTGGC	180
TGGCCTAAAA	ACCTAAATAT	ATGATGAAGA	TTGTAGGACT	GTCTTCCAA	GCCCCATGTT	240
CATGGTGGGG	CAATGGTTAT	TTGGTTATT	TACTCAATTG	GTTACTCTCA	TTTGAATGA	300
GGGAGGGACA	TACAGAACTC	GAG				323

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAATTCCGCC	AAAGAGGCCT	AGGCAAATCA	GAACCTTAA	TTTGTGTTCAT	CCTTATTTTA	60
TTCTTAAAT	AAAGAATTTC	ATTTCAAATA	CGGATTAATT	TTTTTCTGG	AAAAAAACAC	120
ACTGTAAAAC	ATAATTTC	ACCTTTAAA	ACGTTTTACA	ATTATCCCA	TCTTCTAACCA	180
AGTTATGATA	CTCATACCTG	CCGAGGTTTC	TCTAAATTG	TCGCTGGTCT	TCTTTTCCCT	240

CCATTTCAA GGCTTAAAGA TTTTACCAAT GGTGGATAGT TTCCCCTTTC TTTTGAAGGG	300
AGGTGTTGG GAACCTGCTG TGGGGCCATC TGAGTTGCT ATAGAAGCTT TGTCCAGTCC	360
GTCAACTGAG CGGGAGATGT GGACCCGGAG CGGGCGGCCCTGCTCGAG	409

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GAATTCGGCC AAAGAGGCCT ATAAATATAT AATTGACTTA TTTATTAAAT TTAGGAGAAA	60
AAAAAAAGTTT TCCTTGACAT TCAGCTCTAT TGGATTATT TCCATTTAAT TGCATCATGT	120
GTATGTCCTT GTAAACACT CCATTTCTG TCTTGGTGGG CATCTGTCT GTGTACCTGT	180
GCAGTACACT TTAATCATCA AGACTTCAAA TGCTTTGA GCTATCAAAT CTTGGGAGAG	240
TCCCATCTAG CATCTTAATA ATTATTTTC CAAGTTGTT ATAATTAACT CCTTTAACCT	300
CATCTCATTA AATCAATTTC GTATTATCAT TCTGTGTT TCTGGAAAGC AGCCAATTGT	360
TCAGCTCTTG AATCAGAATT TTCAAAGACT CACCTCTCTT ACCTGGGCTT GCACATATT	420
GTCCTAAGTA ATTCTCTATC CCTTAAACCT CTGAGCCCTC GAG	463

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GAATTCGGCC AAAGAGGCCT AATTTGTAA AAAGGAATAT CATTCTTGA TTTTAGATCT	60
TAGACATCG GCACTGACAT AGAGCTTAGA TATGTTCTTA AGGTAGCTAA GCCATTTATT	120
ATAGGATAGT CAGATAGGAT AGTTCTAGGA TTATAGACC TTTCAGATA CTCTTATCC	180
AGTGAGAGAT GACCTATTT TATTTAAACT TGGTTGGT ATCTTGGAAAT TGGCTTGAAA	240
ATGATTGTT TTTACATTGG ATGTGACGG AAAGTTGTA TCTCAAATGT TTTACCACCT	300
GAAGGGACAG CTCGAG	316

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GTGGACATGG AAGTAGGTGA GGTTGGGGA CCTATGAAGA AAAAAAGAGC CTTTCCACTG	60
GGCACTGAAG TGTGTACACA CACACTGGGG GCAGAGCAGT GTGAAAACAT TCTGACCCAG	120
CACACAAATG ACTTTGGCA AATCATCTNC CTGATCTGTC GGATGTTACG TCTCTGCAGA	180

ATCTGGAGAA AACCAGAAAA CCCAGCTTGT TTGCCCTCAT TTTGGCAGTT TAATTTAGGA	240
ATCACACTGG CTITACATAA ACTCTTTACC AAAAAAAACTG TATTCTGTAT TTTGAAGGCA	300
CAAGTTAACCA TGGGCCAAG GGAAGGAAGC ATTGTATAAC ATTACATAAT AGCTACTCTA	360
TTACTTTAAA ACCTAATGGC AGCCTCGGGC AGAAAAGTCA AAAGGGGAGA GAAACCATT	420
CTGTGAAATT ATCTGATGCA ATCATCTCTT TGGAGACATT GTCAGTTGAC AATGGTTCTG	480
CTTTTCTCT CGAG	494

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 507 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

GAATTCCGCC AAAGAGGCCT ACGGGAGCAG TTCATGCAGC ACCTCTACCC ACAGAGAAAA	60
CCTCTTGTGT TGGAAGGGAT TGATTTGGG CCATGTACAA GCAAATGGAC AGTGGATTAC	120
CTAAGCCAAG TTGGAGGGAA GAAAGAACTA AAGATTCACTG TTGCTGCAGT TGCACAGATG	180
GACTTCATTA AACTTTACCT TTTGACCAGT TGGTCCAGAG GGCAGCTGAA GAGAAACATA	240
AAGAATTCTT TGTTTCAGAG GATGAGAAAT ACTACTTACG GTCACTTGGA GAAGACCCCTA	300
GAAAGGATGT TGCAGATATC AGAAAGCAGT TTCTTGTGT GAAAGGAGAT ATTAAGTTTC	360
CAGAATTCTT CAAAGAGGAA CAGTTCTTT CCAGTGTGTT TCGAATTAGT TCACCAGGAT	420
TACAACTATG GACTCATAT GATGTAATGG ATAATTGTT AATACAAGTG ACAGGAAAAAA	480
AGCGTGTGT ACTCTTCAGT CCTCGAG	507

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

GAATTCCGCC AAAGAGGCCT AGCTTATCCA GTCTAGTAAT TTTTTTGTA TGTGTGCACA	60
GCACAAATAG TTACAATAGT TCCCTTTTT GACATCAAAT TCAACAATAC CTGGCATATA	120
ATTGCTAAAT ACTGTCATCA TTTTCATTAT CATTATCCCC CACATAGTCA TAAATAAGCA	180
CACATGCTAA TCTTCAACTC TTCTTCTATT ATTTGCTGCC TTCTTACCTG CGTTAGTGAG	240
AAAGTGCCTT CAAATAGATT GCCAACAGTT ATATGGCTCG AG	282

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

GAATTCCGCC	AAAGAGGCCT	AGTGCAGTAT	TCACGTGAA	CTTTTAAGTT	TTCAGTACAG	60
TGCTTTTATA	CCTTTAATGC	AATGTTGTTAT	TCATTTGGGT	ACTATTGTGT	AGTATTAGG	120
ATGTATGCAT	GTTTGTAT	ATGTAAGCTT	GGTTGGTGCCT	TTCGCTTTG	TGCTACCTTT	180
CTTGGATTTT	TGTACCAAGAG	ATGTGCTAAA	CTGATGAAAT	ACATTGAGAA	AGTTTCCATC	240
TTATTCTTT	ATATGGGACT	GATGATGTGT	GTTGGGGTAG	ACTGCTCCCTG	CAGAGTTGG	300
AAGAAGTCAC	CAGCAAAGCC	GGCCAATCTC	GAG			333

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTCCGCC	AAAGAGGCCT	AGGTTTCTAG	ACTGGAAGAA	CAAATGAATG	GCTAAAAAAC	60
ATCAAATGAA	CATCTTCAAA	AGCATGTGGA	GGATCTGTTG	ACCAAATTAA	AAGAGGCCAA	120
GGAACAAACAG	CCCACTATGG	AAGAGAAATT	CCACAATGAA	TTAAATGCC	ACATAAAACT	180
TTCTAAATTG	TACAAGAGTG	CCGCTGATGA	CTCAGAAGCA	AAGAGCAATG	AACTAACCG	240
GGCAGTAGAG	GAACTACACA	ACTTTTGAA	GGAAAGACAAG	GAACGCNAGA	AAAAAGACGA	300
AGAAAAGGTG	AAGGCAAGAGG	AAGAATCAA	AAAAAAAGAA	GAGGAAGAAA	AAAAGAAACA	360
TCAAGAGGAA	GAGAGAAAGA	AGCAACTCGA	G			391

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

GAATTCCGCC	AAAGAGGCCT	AGCTTCTCTG	CTTTTATTAT	TCATTATTTT	TTAATTTTTT	60
GAGATGAAGT	CTCGCTCTGT	CATCCAGGCT	GGAGTGTGGT	AGCCCCATCT	CAGCTCACTG	120
CAACTTCCAC	CTCCCAGGTT	CAAGTGCATT	GTCTTTTAA	TGTCTATGTG	AAGGATTCTG	180
AGCTGTACGA	GTTCTGCC	AAATCTGCAC	TTGGGCCTCA	GGATCAGGCC	GCCTCCCCAT	240
CAATCTGGTG	GATGCCAGTT	ATAACCTTG	CCCTGCACCC	CATCCACACT	GTAGTTCA	300
AAAAATCAAC	AGTCAGCAAT	CATATCACAA	GCAC			339

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAATTCCGCC	AAAGAGGCCT	ACGAGTCAGC	ATCTAGACTC	AGCTCCTCT	TCCCGCCTGC	60
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CCTCACACAT GCGTGCATTC ACTCTCTGT CCAGGCTCAT GTCCTTGTGC CCGCTTGCTG	120
CTTGCCTCC TTGCTTGTGCT CACCCACTCT CTGTCATTGT CTTGCTTACT	180
CAGGCTCACC CTATCAACTC GAG	203

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAATTCGGCC AAAGAGGCCT AGTTGAATTA TTGCCACATG TTAGGAATGT GGAAGGTTGC	60
TTGGATAAAAT GAGAAAAGAA AGAAAAGAAT GCAAGTAATG TCCTGCTGGG GTAGTGCAGT	120
CCTCGAG	127

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAATTCGGCC AAAGAGGCCT AGATCCCACG AATTTAGGCT CAGAAGCATC GCTCCTCTCC	60
AGCCCTGCAG CTATTCACCA ATATCAGTCC TCGCGGCTCT CCAGGGCTCC CTGCCCTGAC	120
CTCTTCCCTG GGTTTTCTGC CCCAGCCTCC TCCTTCCCCC CCCCCCTATA TCCCTCGAG	179

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GAATTCGGCC AAAGAGGCCT ACTGGAATCA CTAAACTTIG TCTCATTGTT TTTCTCTTCC	60
ATCAAATATC AATTTGGAT TCAGATCCAG TTTTTTCTT TCAATTATTT CTGCCTTTA	120
AAATAATACT ACCTCCTTCC TCCCACAAATT CATTTCAGCT TGTGTTAGTT CCTTGGGTT	180
TATATTTTT CTTCTAGTA TTACAAATAA TGCAACAATA TTAGGTTATA AAACTTCCA	240
TACAACTTTT ACTGCCACTC ACAGGTTTT CAATTGTTT CATTTCATG TACATTAAA	300
TAATGTATAT ATTAGGGATA CTCGAG	326

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GAATTGGGCC	AAAGAGGCCT	AAATATGAAA	AGCTGTCTAT	ATCTACCCAG	CCAAACCATC	60
TCCAGCTTTT	ACTTTTATTG	AGCAAGTATA	CGTTATTAT	TTAGTCATCC	ATTCAATTCA	120
TTACTCATTT	ATTATTTTTT	TTTCAGCTT	ATTTCTGCTT	TCATCTTAAT	TCCTCTCTTA	180
AACTTTTGG	TATCACATTG	GTTCTCCCTG	ACCTCCACCA	CTGTAACCTG	ACTTAAGTTA	240
AATGTTTAAT	TTATTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	TTTTTTTTT	300
TTTAGGTAGA	GAAGATGTCT	CACCATGCTG	CCCACTCGAG			340

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAATTGGGCC	AAAGAGGCCT	ACTTTCTTCC	TTATTCCTACT	TCTCTTTTTT	TCTTTGGTTC	60
AACATCATGT	TTGTGAAAGT	TTCATGCATA	TCGTTGCAAG	TATTTGTATT	TCATTCAATT	120
CTATTGTTGT	ATAATGTTAC	ATTGCATGAA	TATGCAGCAA	TTTGTCTAC	TGTAAAAAGC	180
AATAAGGATT	TAGTTATTTC	CAGGTTGGAC	ACAAATAATT	TTGCTATGAA	GGGTCTCGAG	240

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GAATTGGGCC	AAAGAGGCCT	ATAACTATAT	AGCCTAGAAT	TTTCTCTATT	CTGTTATTAA	60
GCCTCTATCA	CTATTCTTIG	ATTCTAGGTT	TTATAATCCA	TTCTTTTTTA	TAACAACCTG	120
TTCTTGTTT	ACTTTTCCCT	ATTTTGTTT	TATACCCATC	TATTCCTTTT	TAGGATCTAT	180
TCTCCACTTT	TAACTTTGAG	GATTCTAAA	TACTTACTTT	AAAGTTATT	TTAACCTGTT	240
CTATTTTGT	TTTGTCAGG	AGCGAATTG	CCTTTTTAT	TTGGCTGTT	TACCATGCTT	300
TTTGAATT	TGTTTGTAG	GCTTCTCGAG				330

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

GAATTGGGCC TTCACTGGCCT ACTCTACTCC AAGTAGGAAA AGGCCAGGAG GTCCTGTTAA	60
AGGATGCACT CAGAGCCCG GCTCCCTAAC GTATGAGAGT GCTAACCGAC AGGTGTAGAC	120
TTTCAGGAG TGAAGAATGA GGCAGGCATT CCAAACCTGG ACCTTCATCA CCTTTGTTT	180
CATCTAAGA CAATTCTGAG GGACTGTTT GGAGCGTGTC TGGAAAGGTGA ACGTTGAAGA	240
AGAGTGTGGG CTTTGATGTG ACTCAGTTGA ATACTCGAG	279

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GAATTCTCAT GAAACTCTCA GCGGAAAGCT ACAAGGAAAC ACAGATGGTG AAGATTAAG	60
AGGAACCCAT GGAGGTTGAC ATCCAGGACT CCCATGTCTC GATATCACCC AGCCGGAATG	120
TTGGCTACAG CACTTTAACG GGGCGAGAGA AAACCGAACCC TTTACAGAAG ATGCCAGAGG	180
GCAGAGTACC CCCAGAGAGA AACCTCTTCA GTCAGGATAT CTCTGTGAAA ATGGCTTCCG	240
AGCTCCCTTT TCAACTGTCA GAAAAAGTGA GCAAAGAGCA CAATCATACA AAAGAAAACA	300
CCATCCGGAC CAATCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GAATTGGGCC TTCACTGGCCT AGAGCAACAT AGTGAGACCT CATCTCTACA AAAAATAAG	60
AGAAAATTAG TTGGGGGTGG TGGCGTGCAC CTATAGTCCC AGCTACTCAG GAGGTTGAGG	120
TGGGAGGATC ACTTGAGCCC AGGAGTTTGA GGCTGCAGTG AGCTGTGGTC ATGCCACTGC	180
ACTCTAGCCT GAGTGCACAGA GCAAGATCCT GTCTCAAAAA ATAAAGTAAA ATAAAATAAT	240
CAGTCACAA CAGTGTAGTTG TCTTCAAGCT GCCCTCTCTC TCGGCTCTCA AGGCAGTTG	300
TGAAGTGTCT AGGATAGGAA TTTTCCAGAA GGGCTTGCTC GAG	343

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

GGAAGATGTG CCAAAGTTCA GAAAACATAA TCTTATCTGA TCAGATTAAA GATCACAAC	60
CCAGTGAAGC CAGATTTCT TCAAAGAATA TTAAGGATTG GCGATTAGCA TCAGATAATG	120
TAAGCATTGA TCAGTTTTG AGAAAAAGAC ATGAACCTGA ATCTGTTAGT TCTGATGTTA	180
GCGAGCAAGG CAGTATTCAAT TTGGAACCTC TGACTCCATC CGAGGTACTT GAGTATGAAG	240
CCACAGAGAT TCTTCAGAAA GGTAGTGGTG ATCCTTCAGC CAAGACTGAT GAAGTAGTGT	300
CTGATCAAAC AGATGACATT CCTGGAGGAA ATAACCCNA CACTCTCGAG	350

(2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GAATTCCGCC TTCATGGCCT ACTCGCGGTC TGTTAGTAGT ATAGTGATGC CAGCAGCTAG	60
GACTGGGAGA GATAGGAGAA GTAGGACTGC TGTTGATTAGG ACGGATCAGA CGAAGAGGG	120
CGTTTGGTAT TGGGTTATGG CAGGGGGTTT TATATTGATA ATTGTTGTGA TGAAATTGAT	180
GGCCCTAAG ATAGAGGAGA CACCTGCTAG GTGTAAGGAG AAGATGGTTA GGTCTACGGA	240
GGCTCCAGGG TGGGATGAGC GGGCCAAGAT CGATGATCCC ACAGACTCCA AGCCTGAGGA	300
CTGGGACAAG CCCGAGCATA TCCCTGACCC TGATGCTAAG AAGCCCGAGG ACTGGGATGA	360
AGAGATGGAC GGAGAGTGGG AACCCCCAGT GATTCAAAAC CCTGAGTACA AGGGTGAGTG	420
GAAGCCCCGG CACCGTCTCG AG	442

(2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

GAATTCCGCC TTCATGGCCT ACAGAAAGTA AGTTGGAACC ATGTAAGAAA AAAAGACACA	60
AATAAAACTA GGAAAGTGGC ATGGAGCTAG GCGTGAAAGTT GCTGCTCAGT TTACATGTAT	120
GAAGTTCTGT GTGGACTTAA GCTCCTACTT CAGTCATTTA TTGTATGACT TGGACAAGTT	180
GCCAAACATC TCTAATATTC ATTCATATTT GTAGGGTAAA AGGATGAGTA ATATGTATCT	240
TTAGTGTATA AAACATTTAC AGACAACCTCG AG	272

(2) INFORMATION FOR SEQ ID NO:104:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 290 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

GAATTGGCC TTCATGGCCT AAGACACCAG CGAGCCCAGG CAGGTAATGG AAGCACTGT	60
AGCTGACTGG ACCTAAGAAG CAGTGGCACG GGTGCCAGGC ACCCCAGCTG ACCTGCCTTG	120
GTGCTCAGAG CAGCAGGGCT GGCCATGGTC AGGGAGTCTG GGGAGGTCAT GCTCTGTCCA	180
CAGGGTTCTA GCCAGCTTCT GCCAAATTGT CTGTTTTTC TCAAGAGAAG CTGGGAAGGC	240
CAGTTGTGGT GTCTCATACC TGCAATCATA GCACTATGGG AGGACTCGAG	290

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

GAATTGGCC TTCATGGCCT ATGAAAATTG GGAAGAAGAA TCCAATGAAA GTGGTAGCCC	60
TTTTGACCCCT GTTTTGAAG TTGAACCTAA TCTCTAACGA TAACCCAGAG GAACATGTAC	120
TGAAGGTAAT TCCTGAGGAT GCTTCAGAAT CTGAGGAGAA GCTAGACCAA AAAGAGGATG	180
GTTCAAAATA CGAAACTATT CATTGACTG AGGAACCAAC CAAACTAATG CACAATGCAT	240
CTGATAGTGA GCTTGACCAA GACCGATGTG TTGAGTCAA AGACGGTGCT TCTCCATCTG	300
AGAGTGGGCC TGGATCCCAA CTCGAG	326

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GAATTGGCC TTCATGGCCT ATGGCAATGG TGGTCGTGGT GCTGGGTGGG ATGNGGTCTT	60
CATCCTCTTC CTCCAGGAAG GATGCCCTCG GGATATGGCT GAAGGCCTCT GGGTGCAGCC	120
TGGCCAGTTT CCCTTTCAAGC GTCCCTGATAC GGGGAAAGAT GATGTCCAGG TCCCGTTTCA	180
TCTCTACTAG GGTCCCTCGT TGTTGCAGGA AGCGTTGCT CATTGCTGC AGGCGGGCAT	240
TGGACAGGTT GTTGAAGTTG AGCAGCATCT CATTGCTCTT CTCAAAGCGG TCCAGCATGT	300
TCTTCTGGGA CAGGATGATG GCGTTGACAT CATCTGTGTT CACCATGCTC AGGATGCGGC	360
CGCAGAAGAC CCTCGAG	377

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

GAATTGGCC TTCATGGCCT ACATGACACC ACCTGAACGT CTCTTCCCTCC CAAGGGTGTG	60
TGGCACCACC CTACACCTCC TCCTTCTGGG GCTGCTGCTG GTTCTGCTGC CTGGGGCCCA	120

GGGGCTCCCT	GGTGTGGCC	TCACACCTTC	AGCTGCCAG	ACTGCCGTC	AGCACCCAA	180
GATGCATCTT	GCCCACAGCA	ACCTCAAACC	TGCTGTCAC	CTCATTGGAG	ACCCCAGCAA	240
GCAGAACTCA	CTGCTCTGGA	GAGCAAACAC	GGACCGTGC	TTCTCCAGG	ATGGTTTCTC	300
CTTGAGCAAC	AATTCTCTCC	TGGTCCCCAC	CAGTGGCATC	TACTTCGTCT	ACTCCCAGGT	360
GGTCTTCTCT	GGGAAAGCCT	ACTCTCCCAA	GGCCACCTCC	TCCCCACTCT	ACCTGGCCCA	420
TGAGGTCCAG	CTCTTCTCTC	CCCAGTACCC	CTTCCATGTG	CCTCTCCTCA	GCTCCCAGAA	480
GATGGTGTAT	CCAGGGCTGC	AGGAACCCCG	GCTGCACTCG	ATGTACCCAG	GGGCTGGCGTT	540
CCAGCTCACC	CAGGGAGACC	AGCTATCCAC	CCACACAGAT	GGCATCCCCC	ACGCACTCGA	600
G						601

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAATTCGGCC	TTCATGGCCT	ATTTTTTTTT	TTTTTATCAA	AAGTTTGTTT	TATTTCAAT	60
ACAAGATAAA	TACCATGCTT	GTACTAGTG	CAGTTCTCGA	G		101

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GAATTCGGCC	TTCATGGCCT	ACAGAATTGG	AGGCATGATG	AAGACTCTGC	TGCTGTTTGT	60
GGGGCTGCTG	CTGACCTGGG	AGAGTGGCA	GGTCCTGGGG	GACCAGACGG	TTCAGACAA	120
TGAGCTCCAG	AAAATGTCCA	ATCAGGGAAAG	TAAGTACGTC	AATAAGGAAA	TTCAAAATGC	180
TGTCAACGGG	GTGAAACAGA	AAAAGACTCT	CATAGAAAAA	ACAAACGAAG	AGCGCAAGAC	240
ACTGCTCAGC	ACACCTAGAAG	AAGCCAAGAA	GAAGAAAGAG	GATGCCCTAA	ATGAGACCAAG	300
GGAATCAGAG	ACAAAGCTGA	AGGAGCTCCC	AGGAGTGTGC	AATGAGACCA	TGATGGCCCT	360
CTGGGAAGAG	TGTAAGCCCT	GCCTGAAACA	GACCTGCATG	AAGTTCTACG	CACGGTCTG	420
CAGAAGTGGC	TCAGGCCCTGG	TTGGCCGCCA	GCTTGAGGAG	TTCCTGAACC	AGAGCTCGCC	480
CTTCTACTTC	TGGATGAATG	GTGACACTCG	AG			512

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GAATTCCGCC	TTCATGGCCT	AAATTATTA	AGGTGACAGT	ACACAGGAAA	CATTACAATT	60
GAACAAATGCC	TCAGCTATAC	ATTTACATCA	GATTATTGGG	TGCCATTATTG	TTCATCATTT	120
CTCGTGTCA	AGGACAGAAT	CTGGATAGTA	TGCTTCATGG	CACTGGGATG	AAATCAGACT	180
CCGACCAGAA	AAAGTCAGAA	AATGGAGTAA	CCTTAGCACC	AGAGGATACC	TTGCCTTTTT	240
TAAAGTGTCA	TTGCTCAGGG	CACTGTCCAG	ATGATGCTAT	TAATAACACA	TGCATAACTA	300
ATGGACATTC	CTTGCACATC	ATAGAAGAAG	ATGACCAAGG	AGAAACCCACA	TTAGCTTCAG	360
GGTGTATGAA	ATATGAAGGA	TCTGATTTTC	AGTGCAAAGA	TTCTCCAAAAA	GCCCAGCTAC	420
GCCGGACAAT	AGAATGTTGT	CGGACCAATT	TATGTAACCA	GTATTTGCAA	CCCACACCGC	480
TCGAG						485

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GAATTCCGCC	TTCATGGCCT	ACACACATTC	TGAGCTGTAT	ACGTTAACCC	AAAGTCTGCA	60
TTCAAAGTGG	AAATTATAACT	GGGCAGTGA	TGAGTTGCTC	AGTCCATCTA	TTAACCATAC	120
TCTTTAGGC	TTTTTATTGC	CTCTAATTGT	TGTAATAATT	AACATTTCC	CAGGAAGTTG	180
TTTACAGAA	GAAGGGGCCT	TAGCGGCTTT	CAACTTTA	GAGATAAGTT	CAACTTTGTG	240
GATTGACCAAC	AGCACATCTT	GTTTAGTAGT	GAGCGGGAGC	CATATGAATC	CTCTAGAGAC	300
ACAGCCGTGT	CTGAGATGGA	CATTGCCAAC	ACAGCTCGAG			340

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

TTCGGNCTTC	ATGGCCTACT	CTCATAAAAA	TATTCAAAGA	TCAACCCAA	ACGTGCCTGC	60
ANTTGGACA	ATGTNAGCTA	AAGCTATAAA	TGGAACACCA	GTGGTCATGG	ATGATAAAGA	120
TCAATTATTTC	CACCCAATTTC	CAGAGCTGA	TGTGAATGCT	ACACAGGGAG	AAAATCAGCC	180
AGATCTAGAG	GATCTGAAGA	TCAAATAAT	GCTGGGAATC	TGTTGANGA	CCCTCCCTCCT	240
CTTTGTGGTC	CNTCTGGCA	TTCTGTAGTG	CTACACTGTA	CAAACGAGG	CATCTGAGTT	300
ATAAAAGTTG	TGAGAGTCAG	TACTCTGTCA	ACCCAGAGCT	GGCCACGATG	TCTTACTTTTC	360
ATCCCATCAGA	AGGTGTTCA	GATACATCT	TTTCCAAGAG	TGCAGAGAGC	AGCACATTTT	420
TGGGTACCAAC	TTCTTCAGAT	ATGAGAAGAT	CAGGCACAAG	AAACATCAGAA	TCTAAGATAAA	480
TGACGGATAT	CATTCCATA	GGCTCAGATA	ATGAGATGCA	TGAAACACTC	GAG	533

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

GAATTCTGGCC	AAAGAGGCCT	AGAAAATAGA	AAATCAGGTA	GCTATGTCAT	TTTATAAGCA	60
TCAGTCCCTCA	CCAGATTTGT	CAAGTGAAGA	AAAGTAAACA	GAAAAGGAAA	TTAAAAGGAA	120
AGCTGAAGTT	AAGAAAACCA	AAGCAGGAAA	CACCAAGAA	GCAGTGTTTC	ACCTGAGAAA	180
GAGCACAAGA	AACACAAGTA	ATATTCAGT	GATTTGGAA	CCTGAAACTG	AAGAAAGTGA	240
AACAGAAAAG	GAAATTAAAAA	GGAAAGCTGA	AGTTAAGAAA	ACCAAAGCAG	GAAACACCAA	300
AGAAGCAGTG	GTTCACCTGA	GAAAGAGCAC	AAGAAACACC	CTCGAG		346

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

GAATTCTGGCC	AAAGAGGCCT	AGGCAGGTAT	TCTTTGCTTT	GGGAAATTCT	TCTTTCTGTC	60
CTCCCTTCCC	TCACCTTTTC	CAAATTCTGG	GCACAAACAGC	AGCTCTCTCT	CTTCCTGTGGC	120
AGGTGTGCAT	CCTATTGGCT	GGCTGGTATT	TCTTGTGTTT	TTTCCCCCTT	ATTCCTTTTA	180
AATGGGGGTG	GGGGTATAAA	AATATGTGTA	TGGGGTACAT	GCAATAATGT	TGAAATGTTT	240
CTTGTGTTT	AATGGATAAT	TAATTGCAA	ATAATTGTTT	TAATTTATAAC	ATGTTTGAGT	300
AAATGCTAAA	TTAGTATTTT	TTTCTAATAT	AATAATGAAT	TTGAAATCTA	GCATTCCTGT	360
AACAAATGTGT	CTATGTTGT	CTGTCTGTGT	CTGTCTAATA	GTAATTAATA	TCTGTGGTCC	420
GCACCCACTC	GAG					433

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GAATTCTGGCC	AAAGAGGCCT	AAGCAAAGCT	TAGCTTACGG	GGAAAAAAAA	AAAAAAAAAA	60
AAGTAGAGCT	TNCCTTGAAT	CTGGAGAAAT	TAAGCACACA	GGTGTCTGC	AATATTAGTT	120
AAGAGACTAC	TGCACCCATC	ATACTGTAGC	TTAAGACAGT	TTCTCTTTT	AGTTTTTTCT	180
AAAATGTC	CATGTCTGTG	TTATGCCACA	AATAACACAG	CCTTGGTAA	CTTTTGGACT	240
AAAAAAAATC	AACTTATTGG	CCAAGCATGG	TGGCTTACAC	CTATGATTGT	AGCACTTTGG	300
ATAGGTCTCG	AG					312

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAATTCCGCC AAAGAGGCCT AATTTTCTTA ACGTGTGCT GCCTTTGGG TTAATTAGAA	60
TTGTAGCATT TCGTTTGAT TATTTTTTG GCTCTTCTAGC TGTTCTCTCA CATTTTTAA	120
AATGGTAACT CTAGGGATTA TAATATGCAT CTTTAATTAA TCAAAGTCTG TTTTACTAC	180
TTCGTGTAAA ATAACGAAC CTTGCATTAA TAGTTACATT TATTCTCTC ATCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

GAATTCCGCC AAAGAGGCCT ACTCAAAAGT AGATGAGCAA TTGGTCAGAA TTGTTAGAGG	60
ATATTATTTG AGCTAAATGT TTCTCTCTC TGTTTCAGTG GTGTATGTGC AAGTGTGTGT	120
ATATGTTTTT TGTTGGGGAC AGTTTCAGGT AGATGGTATG AAGAGGCAGC AGGAGACTCT	180
CGAG	184

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GAATTCCGCC TTCATGGCCT AATTTTCTAA AACCTGGAGA CAAACCACAT AAATACAAAA	60
CAAGTCTGCT TCTTCAAAAT TCTGCTGGTG AGAACTCAGA TATCAGTGAT CTTATTAGCT	120
TTTCACAAG CCAGAACATA ATGGTGACCA TGATTAATGA CAGTGACTAT GTATCCGTGG	180
CTCCCCATAG TCGGGTTTA AATGTGATGC ATTCAAGAAA GGACTATGTT TTTGCAGCTG	240
TTTTCAACAG TACTATGGTT TATTCTTAC CTATATTAGT GAATATCATT AGTAACTACT	300
ATCTTTATCA TTAAATGTG ACTGAAACCA TCCAGCTCGA G	341

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

GAATTATGCT GTGCTGTTT CCTGGACACT CAGAACATCAA CAGGCCTTCC ACCCCATCCC	60
ATCATGTTGA ATTACAAAGT ATTTTGAGCA TCGTTGGTT TGTTCTTTC CACCCATACC	120
TGTGTAGGGC AGCGGTAGCA GTCTTCACAA ATGCATCCTC TTGGACAATG CATTGTAATA	180

TCTCTCTTTC AAATTCTGTT TCACATAGTC ATTTCTCATG TTCTGTTGGA GACCCCAAA	240
AAATTCATTC CACACTGTCA TCCCTTGTC CTAACCAGAA TCTCGAG	287

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GAATTCTGGCC TTCATGGCCT AATGTATGGT AGACAATTT TTTTAAGAC ACAGAGATAA	60
ACGTTTCCT GCTTGGGTA CCTTTCCCTT CCCCTTTAAA AGGAATTAGC TATAGAACTG	120
CTTTGTAAG ATGCTTCTTG ATATTTACT TTTGTTCTT TTCCCTAATC ATTCCCTTTT	180
CACCCCACTC CTCGAG	196

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

GAATTCTGGCC TTCATGGCCT AGTGATTGGG TGCGAGGAA ACAGGAACCA GAGAAGGGTC	60
ATCTCAGCTG CCTGTCCCAC TCCCTATGCT TGGTGTACCG TCGGCCATAG TCTCGAG	117

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

GAATTCTGGCC TTCATGGCCT AGTAAGTGCT CTGAGTATAT TAGGAAAAGG AAATCTTATA	60
CATAAAAATC AAAGCTGTT CTAATTTTC CACTAGTGAG TCAGTCTATT AACATTACTC	120
ATGGTAGTT TTGCCATACA GAATTTAAT TTTTTATAT TATTTTGCGC TTGTTATTA	180
TGCTTACAAG TCCATGGGGA CCCAAAGATC AGAAAAGATT CATCTGTACT CGAG	234

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

GAATTCCGCC TTCATGGCCT ACGGAACGAA CATTGGCTCG GCGGTGGTGA TGCTAATTCC	60
CACTGTCATG TTACAGTGA TGGCCGTCTT TTCCCTCATC GCCCTCAGCA TGTTTCATAA	120
ATTTTACCGG GGAAGTGGGG GGAGTTTCAG CAAAGCTCAG GAGGAGTGGA CCACAGGGC	180
CTGGAAGAAT CCACATGTGC AGCAGGCAGC CCAGAACGCA GCCATGGGG CAGCCCAGGG	240
TGCCATGAAT CAGCCAAGAC TCGAG	265

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

GAATTTGCCA CACCATGAAG CTCTTGTGGC AGGTAACTGT GCACCACACCTGGAATG	60
CCATCCTGCT CCCGTTCGTC TACCTCACGG CGCAAGTGTG GATTCTGTGT GCAGCCATCG	120
CTGCTGCCGC CTCAGCCGGG CCCCAGAACT GCCCCTCCGT CTGCTCGTGC AGTAACCAGT	180
TCAGCAAGGT GGTGTGCACG CGCCGGGGCC TCTCCGAGGT CCCGCAGGGT ATTCCCTCGA	240
ACACCCGGTT CCTCGAG	257

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

GAATTCCGCC TTCATGGCCT AGGAAAGATT CGTGTGTTAC TTTAATAAAC CTGAAAGAAC	60
TGTCGTTTT CACTGCCTAT AGGACCACTA CAAAGCCGCA AAGAAAAATT AGACTTGT	120
CATTTTATAA CAACAACAAAC TGCTACTACT GCTACTAGTT AGATACCGTT TGCTCATTTA	180
TAACAATCTC AGTTGGTAGG ATGAAGCTTA AACACTTGGC ATTCACTCGTC TTTTCAGTC	240
CTCTCGAG	248

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

GAATTCTGGCC	TTCATGGCCT	ACTGTCTTT	CATGCAGATT	TCATATTGTC	TTTGTCTTT	60
TCATTGCTTC	TTGACCTTCC	TGGCAGGTGT	CGCTCAGTTT	CTTCCCTGTT	CCCTTCCTGT	120
CCTCTCCACA	CCTGCTATCC	CGTCCCACTC	CCATCTACCT	CCCGGAAAGC	CAGCCCTGCA	180
TGCTGAGTTT	GTGACCTGCT	TCATTCCCAT	TTCACTTCTA	GAGGGTTTAG	AGGTGACCTG	240
GAACCGTTCC	CTTCTCCCTCT	CCTACCCCCCT	CCTCTGCAAC	ACCAAGAGGC	CTGGAGGGGC	300
AGACAGAAAG	CAGCCAGCCA	CGGCGGGAAG	TCTCGAG			337

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

GAATTCTGGCC	TTCATGGCCT	AACTTATTC	TTTTGTTGAT	TGCCCTGTCTT	TCTTTTTCTT	60
TCCCTCCCTC	CCTCCCTCCT	TCCCTCCCTT	CCTTCCTCT	GTAGAGATGA	GGTTTCACCA	120
TGTGGCCAGG	TTGGTCTCTGA	GCTTAAGTGG	TCCTCGACCC	TCAGGCTGGC	AAACTGCTGG	180
GATTACAGGT	GTGGGCCATC	ACGCCCTGGCC	TTACAGTAAA	TTCTTGATAA	ACAACCCAGC	240
AACACACCTC	GAG					253

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

GAATTCTGGCC	TTCATGGCCT	AGGACGGGGG	ACTCAGGTTC	TACACTGGAA	CCTGGGGTCA	60
TGTATCATGT	ACCAAGGTGGG	GAGAAGTGT	GCAAATCTCA	GTGCCAATT	GAGGGAAAGC	120
CAGTCATTCC	AGGAGAAAGAG	CTGAGGGGAA	AGAGCTGTTG	ACTTCATAA	TGCAGTCTTA	180
ATTATCCAGT	CACCTCTCTG	CCACATGGCA	GAAGCCAGGT	GGCAGTGATG	GTGGTGGGGG	240
AAACAAAACA	CACAGTCCT	GGCAAGCCCC	ACCGGGAAAG	GAGGGCTCAG	AAGCGTAGC	300
GGGTCCGGAT	ATCCTCGAG					319

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

GAATTCTGGCC	TTCATGGCCT	ACAATAAAAG	CCCATAGGGA	AGAGAGAGAG	GATATAGGG	60
AACAGAAATCA	GATGTGTAAT	ATACTTGGCA	CAGGAAAAAA	ATGGATTAA	AAGACAAAAA	120
TGGAGGTCCA	GGTAGATGTA	ATTCACACAG	ACTGAAAGTG	AGTTCTGGCT	TGTGTAAC	180

ACATGAGATT GGATTTGACC CCTTGGCTCT CAACTGTCCC CTTAGATCTA GAACTGCTCC	240
TTGGTGGCCA TTAGATCGAG TCAGTTTGAG TCTGCATCAC TTAGTTATTG GGAATTTCCTT	300
TTTGGAAAC AGGAAAATTT TTTAGAGTAA TTTGGCGTAC GGCTCGAG	348

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

GAATTCCGCC TTCATGGCCT AGGCACAGTG AAACCCGTGG AAATTCAAAG GTGAGCAGGA	60
CAGTGGTCC TGTATCTTGA TCTTTACGGA TCTTTCTCTT CTTGAATCCT CACAGCACCC	120
ATTTTATAGA CACGAAGACT GAGGCCGAA AGTTCTCTCT GACTCTGAGC CTGGCCTCTT	180
TGCTGCCCTCC CGTTGTCCTG TGAGGCTGTG TGGTCACAGC ACCCAGGACT TGAGAGGAGT	240
GAAGTTCTTC CTCACCCCGC AAAGGCTTC TGAGGCCCTAC TGTGTGCCAG GCCAGCCCTG	300
CTCAGTCTGG GGCAGATAAAC ACAGGGCAGA TTCTGAAAGC CTGTTGAGG GAAGTTCTAG	360
GCCTGCAGGA GCTGAGAGGA GACCCCTGGAG AGGAAGGGAG TCAGGGCCAG CTTCCTCGAG	420

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GAATTCCGCC TTCATGCCTA AGCTGATGGA GACTGTAAT GAACCAGAAA CAGGTGAAGT	60
GAGCAAGAT GCAGTCATTG TAAAGCAGGA GAAAAATAAT GAATATTGCC TTCAAGGATAT	120
TGATGATAAA TTGTCAGAAT CAGCAGAGGA TGATGGTGAAT GATGATACCA ATGATGAAGA	180
TGATGATGAA GATAGTAACC CTAAAAGAA TACTCAGGGC CCACTAGAGT TAATGGCAGA	240
ATTTCTGAGA GCAGAAATGG CCCGAGAGTA CCAGCTGGCA AAAAAATTAT GTCAGATGAT	300
CCTAATCTAT GAACCGAGAA ATCCTGAGGC CAAGGAGTTT TTCACACTTA TTGAAGAAAT	360
GTTGCTGATG GAGAAAATC AGAATCATGA GCAAGACGGT GAAAACAGTG ATGAAGACAG	420
CAGGGGGCTC GAG	433

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

GAATTCCGCC TTCATGGTCT ACAAAATCAA CTGCAAGCAG CCATCATCAG TTTGGAAGAA	60
GCTTTGGGAA GCCTTCAAAG AAAAACCTCG GTATCCACCA AGTCAGGCTC AAGCAGCTCT	120

TCAAGACAGT	CCCCCTGAAG	AGTACTCCTA	TAAGAAATCA	ATAAGAAACC	TGTTTAAAAA	180
CATTCTTTT	GTCCTTCTGT	TGATCACTA	TGGTATCATG	ACTGGTGCCT	TTTATTCACT	240
CTCAACGT	TTAAATCAAA	TGATATTGAC	ACAACTCGAG			280

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GAATTCGGCC	TTCATGGCCT	ACCGCAGCGG	CAGGTGTGCA	CAGGAGGTTG	TCCACTTTGT	60
NCTCTGA	CGCGGTGCA	AG	ATGGTTTCT	CTGTCAGGCA	GTGAGGCCC	120
CTGAAGAAGT	TTTACTGACG	TTCAAGATAT	TCCTTGTCAT	CATTGTCCTT	CATGTCGTT	180
TGGTAACATC	CCTGGAAGAA	GATACTGATA	ATTCCAGTTT	GTCACCCACCA	CCTGCTAAAT	240
TATCTGTTGT	CAGTTTGCC	CCCTCCCTCA	ATGGTACTCC	AGAGGTTGAA	ACAACAAGCC	300
TCAATGATGT	TACTTTAACG	TTACTCCCTT	CAAACGAAAC	AGAAAAAACT	AAAATCACTA	360
TAGAAAAAAC	TTCAATGCA	TCAGGCGTCA	ATCTCGAG			398

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GAATTCGGCC	TTCATGGCCT	AGGGCGATGG	TGGGAGGAGG	ATCCCTAGTG	CTCAGTCGGG	60
CTCCACCA	AG	ACCA	GGACT	GAGACTCTCG	GTTCAGGTA	120
TGGAGTTTG	GACACAGATC	CTCCTGGCCA	GAGAAGGATG	CTTGAGAATC	TGAGATTTCAC	180
ACAGCTGTAT	TAGGTTGTCC	ACGATGACCG	GGCAGTAGGT	CTCTCTCTTG	GGGATTTCT	240
CAGTGGCTG	CCAGAGACGG	CGGTGAGAGA	TCACATTCAG	AACGCACTCG	TCTTGGTTCT	300
CTATGTGGTT	CCTTGGATCA	TCAACAAAGG	TAAGCACTTT	CTCGGAAAGG	CCTTCTATTA	360
ACTTGGTCTT	GGTGAGCCAG	AGGGCCTGCT	TTACACCCCTC	GAG		403

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

GAATTCGGCC	TTCATGGCCT	ACTCCATTT	TCGAATGGCT	TATTTAGGCC	CAGCTCTTGC	60
GTTTGCATTG	TCCCTTCAGG	CCCAGAACCT	TCTCACGTCA	TCGTCACCA	GCCTAGCTTC	120
TGCATCTGGT	CAGCCTTTA	AGGCCAGCT	TTTGCCTCAT	AAACTCAGCT	CCTGTTTAAT	180

GGCGGCCCTCC CGGGTCCCAC TCGAG

205

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

GAATTCCGCC AAAGAGGCCT AGTTTATTA CTTGGTTAA GACATCAGTT ATTTTACTCT

60

TTGATAATTTC ATTATCTAGA TAATGGTTAC TTGTATTGT CTGTTCTCG AG

112

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

GAATTCCGCC AAAGAGGCCT ACACAGAGCC CTTCACTACT TTTAATTCTT CTTAAATTGG

60

TGGTTCATGT TAATTAATT ATTATTATT TTTTTGAGA CGGAACCTCGA G

111

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GAATTCCGCC AAAGAGGCCT AAAGATGTT TCCATGAGGA TCGTCTGCCT GGTCTTAAGT

60

GTGGTGGCA CAGCATGGAC TGCAGATAGT GGTGAAGGTG ACTTTCTAGC TGAAGGAGGA

120

GGCGTGCCTG GCCCAAGGGT TGTGGAAAGA CATCAATCTG CCTGCAAAGA TTCAGACTGG

180

CCCTCTGCT CTGATGAAGA CTGGAACCTAC AAATGCCCTT CTGGCTGCAG GATGAAAGGG

240

TTGATTGATG AAGTCAATCA AGATTTACA AACAGAATAA ATAAGCTAA AAATTCACTA

300

TTGAATATC AGAAGAATCT CGAG

324

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GAATTCTGGCC	AAAGAGGCCT	AGGTCCAGAA	ACATTTAAA	AAAAAAAAAA	GGGGGCTTGA	60
GAAAAGGGCT	TCCAGTGCCA	GGCAGAAATA	TGTTTTCTT	AATAGGGC	108	

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

GAATTCTGGCC	AAAGAGGCCT	ATGAAAACGT	GGATTTGCTT	TGTAAACTTG	AGAATACATT	60
TTGTTGCCAA	CAAAAAGAGA	GAAGAGAAGA	GGAAGATATT	GAAGAGAAGA	AATCGATTAA	120
GAAAAAAATT	AAAGAACTTA	AGTTTTAGA	TTCTAAAATT	GCCCAGAAC	TTGTAAAGTA	180
TCATATTCCA	ATACCATTCA	AAGACAGTGG	AAATATTCT	TTAAATGATT	TCATTTCTT	240
TAAGACCGAT	TATTCATTAT	TTGCTATTTT	CATTTGTTA	TTATATGCAT	GATAAATTCA	300
CAGATACTCT	CGAG					314

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

GAATTCTGGCC	AAAGAGGCCT	AGGGTAAGAC	TAGAGTGT	TAAATCATCA	ATAAAAAGTG	60
GAGAAAACAA	AGGTTATTCA	GGCATTGAAT	TCTAGACCTG	CCTCGAGCCC	TGCCTTCCT	120
TTACTTTTAC	TTTTTTTTTT	TTTTCTTGTG	GAAGAGAGAA	GAACAGAGTG	TTCGATTNTG	180
CCCTATTTAT	GTNTNTANTC	GGGAACAAAC	GTTGGTTGTG	TGTGTTGTG	TTTCTTGTG	240
TTGGTTTTTT	AAAGAAATGG	GNAGAAGAAA	AAAAAAATTG	TCCGCCCTT	TCCTCGATCT	300
CGCTCCCCCC	TTCGGTTCTT	TCGACCGGTC	CCCCCTAAC	CTGCCCTCGAG		350

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

GAATTCTGGCC	AAAGAGGCCT	AGAGAGTCTG	GATGACAAGC	AAAGCTCAAT	CTCAAAACAA	60
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TAATTTTAA AGTAATGATT ATCTTAACCA TTCTTAAATC CTTCTGTCTA GTAGGAATCT	120
TATTCATGGG AGTGTCTGGA AAAGGGACAA AGAGCGGCTA TCTCGAG	167

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

GAATTCGGCC AAAGAGGCCT AGTGTTCAC AAAAGAATTG GAAACCATAG TCCTGAACTC	60
TCCCTAAAGTA GTATAAGCTT TAAATAGCAC TCAATCCATA TTAAGTCTTC TTAGTGTAGC	120
ATGGTGCTC TCATGCGTCT TTCTTATGTT TAAATGGTG TAAATTTAG TCGTTGTCA	180
TTCAGAAAGTG GCTTTGCAAATACAAAATAT CTCGAG	216

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

TAATCTTAC TGGTAAAAAG GATGGAAAAAA TAAATCAACA AATGCAACCA GTTTGTGAGA	60
AAAAAAAAAAA AAAAAAAANC CGAAAAAAA AAAAAAAACA CCTGAATGCG GAAGAGCTCG	120
GCTCCCGTTT AGCATTTTGT ACTTAAGGAA ATAAAAAACC AACAAAGGAT CTCACATTTT	180
CTTAAAAACT GAAGATTGCT GTATACTATT TATTCAACTT ATAATTTATG TTACTCCTTG	240
ATCTTGTCT TTGTCATGA CAAAGCATT ATTAAATAAA GTTATGCATT CAGTTCTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

GAATTCGGCC AAAGAGGCCT AGTCTCTGTT AATCCTACTC TGCTTTAGCC AGAATAGCCT	60
AGTATTTTAT TTCTTATTTA TATATTGAGA TTTCTTCTAA CATTTCCTTT GATAAAAATC	120
TTCTGCTTT TGAAAGTGG TATGTATCAT ATTATTTATGT TTCTGGTGTG TCTCGAG	177

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GAATTCCGCC	AAAGAGNCGT	AGGGAAAGAT	TTCAGCTATT	AATCAACTGG	AGGAAATTCA	60
AAGCCAGCTG	GCTCTCGGG	AAATGGATGT	CACAAAGGTG	TGTGGAGAAA	TGGCCTATCA	120
GCTGAATAAA	ACCAACATGG	AGAAGGATGA	GGCAGAAAAG	GAGCACAGAG	AGTTCAGAGC	180
AAAAACTAAC	AGGGATNTTG	AAATTAAGA	TCAGGAAATA	GAGAAATTGA	GAATAGAACT	240
GGATGAAAGC	AAACAACACT	TGGAACAGGA	GCAGCAGAAG	GCANCCCTGG	CCAGAGAGGA	300
GATTCTCGAG						310

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

GGTGGCCCTTG	GGTCAAGATT	CGCACCATGG	TGGGCACAAA	CCCAGGAGAA	CACTTCCCTG	60
TAAACGTGTT	TTCATGCTGG	AGCCAAGGTT	TTGACTTGGG	TTTGGATTTT	TATTTATTTA	120
TTTATTATTA	TTTATTACCA	GTTGCATCTA	AAGGATGTTT	TGGAGGAGCA	CAGAGTTTGT	180
CTGGTGAGGG	TAGGCTCTGG	GCAGATTTT	CTGTGAGTCT	CCCCTGCTG	CGGCATCAGG	240
ATCATCCCTG	GTGCCCTGTG	GTGGCACCAAG	GTGGCTGCC	ACCCACAGGC	GTGGCCTTCA	300
CAGTGGGGGC	CATCTCAGCC	TGGGGTAGCG	ATCTGCCTCC	GACCTGCCTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGCCTGCATC	GCAACAGCCA	GGAGGGCCAG	GCCACCCAG	GCAGGGAGCA	GTGGGCTGGC	60
AGCCACCCCTG	GGCACAGAAAG	AGCAGACGCA	GACAGTGTG	GGCAACGAGG	GGCTTCTTC	120
ATGGGCCCCG	CTGCCCTGTG	CCTCCCCCA	GGTCCCCACC	TTCTAGGGTT	AAAGTGCAGC	180
TGGGAGGGAG	GAGGCAGGCA	GAATTGGGA	GCTAGAGAGA	GCCCAAGTGA	ACCCCTGACTG	240
TCCACGCAAG	TCCCATGTCC	TCCTCGTCCT	GGAGTTCCCTC	GAG		283

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

GAATTCGGCC TTCATGGCCT AGACCTGCCT CGAGTTCCCTT TTGTTATTC CCTGCATCTT	60
ACAACTTAA GCCCTGGTC CCTGCTATAATAAATAAT AATCAACTTT ATAAAGAGCT	120
TACAATATGC CAGATACTGT ACTAAGTGT TTATATTTTT TTTTGGGTG GGGGGTGGCT	180
GTGGGGCAGT GTCTCGCTCT GTCACCCAGG CTGGAGGGCA GTGGCACAGT CATGGCTCAC	240
TGCGCCCTTG ACCTCCCTGG CTCAGGCCCTC CCGCCTCAGC CTCCCAGGTG GCTGGGGCTA	300
CGGGCGTGCA ACATTCTCGA G	321

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GAATTCGGCC TTCATGGCCT ACGTAATTCT GGAAAAGTGA ATACTTGTGA AGAGTCGTCT	60
TGAATGATTG GTAAAAAAATC CTGTTCTTAT ATTCAACGAG TTTCAATCT TTGTCAGAGG	120
AGTATTACCA TTAGATTGAA AAAAAGGGAA ATAAATAATA AACACTTTA AAAAAGACTCC	180
CCATTCTCTT ATTCTCACTT TTAGGAAAAG AGACTGACTA ATATCTCTG CCACAAATAC	240
CGATGTTCTT AAAAATATTG ATGGGACTGC TTTGGCAAC CAGCCCTATT TTGTTTCAT	300
ATCCCTTTT GCTCCCATCT TTCCAAACTC ATAAACTCGA G	341

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAATTCGGCC TTCATGGCCT ACTCGCCTCT ACTAAAAATA CAAAATTAG CCAGGCACGC	60
GCCAGGTGGT GCGCACCTGT AATCCCAGCT ACTAGGGAGA CTGAGGGGG AGAATTGCTT	120
GAACCTGAGA GGTAGAGGTT GCACATAGCG CCACTCGCCT CCAGCCTGGG CAACAAGAGT	180
GAGACTCTGT CTCAAAAAAA TATATAATA AATAATGAA AAAAATAAT TGTATAACAT	240
CTATACTATA GCCTCGTAAG CATTAGCTAC TTAATATTTT TGGTATATTT AATAATTTA	300
ATACAGCATT TTGATTACT AGTGAACATG AATATTTCC CATAATTGTT AATTATACTT	360
TCCTCTTACA GAAATTCTGT TTGTGTCCCT CACCCCTCAC TCGAG	405

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

GAATTCTGGCC TTCAGGGCTC CTTCTTCCTA GGCTAGTATT TATCCCCTA CATCTGACTC	60
ATTCTCTACT ATCGCTGTTG ATTTCTCTT GGGTACTAAA TCTGTTGAAC ATGTTGCCAG	120
GCTTACTGCT GGTATTATGG GATAGCATT GCCTGATGGC AGCTTCTAAA GGAGACTCCG	180
ATGGCACTAA GCAGTTTCCA AAAGTTTATC TTGCAAGTTC AACCCATTG GAG	233

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

GAATTCTAGA CCTGCCTCGA GATGTTTTTG TCGTTATTTG AAATCTTGC TCTTTTATTT	60
TTCAGCTCCC AGATCCTCTC CCTCTCTTA GCTTTCACTG TGTTTGATAT CAAGAATATG	120
AAATGTGAAT TCCACGGACT CGAG	144

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

GAATTCTGGCC TTCATGGCCT AGGCAGGAAG GAGGCTGGAA TAAATAAAAA TAAAAATAGA	60
CAAGTAAAGAC AGCATAAATA ATACATTTTT AAACATGTCA ACATIGATAA TACAATGAAG	120
ATTTACCATA AAAAGTATCA TATCTAACCA AGATATGCAA AAGATGCATT CAGTAAGCTG	180
TAACCTTGAG AAAATGAACT GTGAAATCAG CTCACCAAGTT CAAGTCACTA GGTTTGCCAC	240
TTGGACCGTC TTGGTTTCAG CGAGCATAGC GAGTGGCTGT AAGAAATTGT CCATGCCACC	300
AATTCCACTG CTACTTGCCCC AGGTGGTCTC GAG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

GAATTCTGGCC TTCATGGCCT AGGAAGTGG ACGGAAGCTGG GTCGCTGCTG GAAGGGAGGG	60
AGGCTGACTC TCTACCCCTC ACCTCTGCAA GGAACGTGAGG CCTGTTAGGG TGCGGCTGTC	120
ACTGGCTACA GGCGGCATCT TTCTGTAAAA AGCTTTTCAG GCATGAAACC CATTCTGTGTA	180
TGGACTGGC TGTGTTGACG GTGGTGCTTG GGCGTTGTGT GCCAGGCCTC TCTGGGTCCC	240

CTCCCTGGCC TTTGCCTTCC TCTCACCTTC TCGAG

275

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GAATTCTGGCC TTCATGGCCT	AGAGTCATAG GTCAGACAC	TTTCTAGGAG CTGTTCA	GTG	60
ATAAAATTAA TAACAGTGAC	TTTGAGTCA AAATAGATT	TTAAAGTACT TGATTTT	CTC	120
TTTGATTTGG AAACATCTT	TTTAGCTTA ATTGAATGA	TCTAAAATAT TTGAAGGATT		180
TTATACTTTA CACAGAGGCA	TGTATTGGA TAATTAGCTT	TTATTAACC CAGGCTTC		240
CGAG				244

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GCGATTGAAT TCTAGACCTG	CCTGAACCCC ACCCTTCAGG	TCCTACTTGG GCTGCCAAAG		60
TCATCTTCCC AAAACATGAC	TTTCCTCAG TCAC	TTTCT TATTAGATT TATCATATT		120
CACATCCCTT CCCTGGCCCT	CAAGGGTGCC	TGTAACCTAG AACCATCTTA	CCTTCCACC	180
CTTGTTTCCA AACCTTCCGC	TTTACTT	AGA CATGCCCTC CATTCCCTC	CCGACCCACC	240
CCCCTCGAG				249

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GAATTCTGGCC TTCATGGCCT	AGAAAAAAAC AAGTAGTTG	GCAAGGAGAG CAGAAAAATA		60
AAATTCCACT GTGTAGGCAT	TTGGAGATT	ACCAAGAGCA ACCTAGAGTC	TGCC	120
GACACTGCAC GTTGTTCCTG	ACACAGAGGA	TGCACTAATT CTATTCCTG	TGCCACCTGA	180
AAAAATCATA ATTTGAGAAG	AGAAA	AGTGTGAACTA	TTTTCCAAA	240
CCCTCACGGA ACCCTGAACA	GGCGTGTCT	CGAG		274

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

GAATTGGCC	TTCATGGCCT	AAGCTTGCTC	ACTCTTCTGT	GTGTTTGAAA	TAATGGTAAA	60
ATACAATAAT	ATTGTCAAGC	ACAGTGGATC	GGAGATTTT	CTTCTCAGGA	CTATTCTGCT	120
TATAGGTCTA	CTTCCTATAG	CTATTTGTC	TTGTCCTCCT	GGTCCTTCTC	TTTCTTCTC	180
TCCTGTGCTA	GATGCTCT	CTTCCTATCC	CTCCCTCTCT	TCCCACCCCC	ACCTCCCACT	240
TCTCTGTTA	TATCCTGATT	TTGGTGGAAC	ACATCCTCCA	GGCTCCCTGG	CACTCGAG	298

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ATGGCTTAAG	GTGCCCNAGC	TTGCCAATT	ATTCCCAGTA	GAATTTTTA	AATGTTAAAG	60
ACAGTAATT	AAAAAAA	AAAACCACAC	TGTTTGACA	TTTACCTCG	TGCTTTGTGT	120
GTGACTAGAT	TATGCACTAG	AATTCATTC	AGTATTCTTC	CAAATAAGTT	ATTTCCCAGG	180
TGTTCGCTGG	TATCTAACCA	ANTANTCAAT	AAAGTATTCT	TGCTAAGTNG	GCCATGAAG	239

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

GAATTGGCC	TTCATGGCCT	AATATCATGA	TCACTGAAAT	TACATCTAGT	GAAACACACA	60
CGTGCTTATC	TGCACGTGTG	TGTAAGTTAG	AAAGAAAAAA	CAAAGGCCTA	ACAGTGATTG	120
TCTTAGTTG	ATAGGATAGT	GGGTGGGATT	TGCAGAATT	TTGTATCTGC	AGAATTTTG	180
CAAAGTGCC	ATTAGTTTG	AAAGAAAAAA	AACCTAAATG	TATAACTTCT	AAAGAGATAA	240
TTTTTCTT	CATGTTTTG	CTACCTATAT	CTAGGAAAAT	AACTTAGAAT	TGTAATTATT	300
TTGAAGCTCT	CCAATTATTA	TGTTCAAAA	TTACAGAAC	AAAAGTCTC	GAG	353

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

GAATTCTGGCC	TTCATGGCCT	ACTTGCTGTG	GCTGACTCGG	TTATTGACTT	TACTTCTTT	60
CTTTTCAGGT	TTTTATGGG	CTGTTCTAG	CCCTGATTCA	GGTGTGTATG	AAATGAAGAT	120
TGGCTCCATC	ATCTTCCAGG	TGGCTCTGG	AGATATCACG	AAAGAAGAGG	CAGATGTGAT	180
TGTAATTCA	ACATCAAAC	CATTCAATCT	CAAACAGGG	GTCTCCAAAG	CAATTTAGA	240
ATGTGCTGGA	AAAATGTAG	AAAGGAATG	TTCTCAGCAA	GCTCAGCAGC	GCAAAAATGA	300
TTATATAATC	ACCGGAGGTG	GATTTTGAG	GTGCAAGAAT	ATCATTATCG	TAATTGGTGG	360
AAATGATGTC	AAGAGTTCA	TTTCTCTGT	TTTGCAAGAG	TGTAAAAAA	AAAATTACTC	420
ATCCATTGTC	CTCCCAGCCA	TTGGGACAGG	AAATGCCAA	CAACTCGAG		469

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

GATTATTCA	TTCTTGATTA	AATGCACTGA	AAAGTAAAGG	GTCTGTTGT	GTCATGTTCA	60
TGAAAATGCG	GTTAGAGAGG	TGCTATTCAA	GTGATTCTGA	AGGCACCCCCA	AGTATATCT	120
GTAATTAAA	GATTACTGCA	AATATCTTA	CTTTACTGTG	GGTTTTAGT	ACATCTGTTA	180
ATTTAGTGT	TCTTGTGTG	TTTGTAGAC	TAGTGTCTT	CCATCCTTC	ACTGAGCTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

GAATTCTGGCC	TTCATGGCCT	AGCATTTC	TTCCTAAAT	TATTGTATCC	ACTAGTTCTT	60
GCCAGTATAA	AGGAATACAA	TTGACTTTG	TGTTTTCAT	ACGCTACAC	CTTTCTAAAT	120
TCACTTATCA	GGTCCAGAAC	TCTTCTACTA	ACAATGCACT	TTTATAAAGC	CCTAACACCT	180
CTCTGATCT	CTGTCTCACC	CTCCCACCTA	TCTCACTGTG	GGATGGAAAG	GAAGTCATG	240
GAAAACACAG	GAGCGCATTC	TAATAATAGC	CCACATGGTA	TACTCGAG		288

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GAATTCCGGCC TTCATGGCCT AGCTCGATCC AAGAAGAAAA ATTAAAATGA CAGCTTTCC	60
CATTGATATA ATCATCTTAC TTTGCTCTC ACAAGAAAATA TGCAATTAGGA ACCTTCATTA	120
TAGGTCCACA GAAATAGCAG AACACAAAAG CGCCCCCTA CCCCCCGCC CCGGTAACCA	180
GAAATACACA GAGGCAGAG	199

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

GAATTCCGGCC TCATGGCCTA GAATTAACCA ATTAAGAATT AATAAATTAC TTATAAAATT	60
AAAAATCAGG AATACCAGGC TTAATGCATT CATTATTCTC ATTTAGCAA CTTTTTTTTT	120
TTTTTGAAAT GCCCACAATG TCCTAGGTC TGAAATACA AAATTACTTG GTACCAGTAA	180
CTCGACTGTC ACCTTTCCAG CCATGGACTT GGTTAGACA AACCCCCAGT CCACGGTTGT	240
CGTCCACTTG CAGTGCCGC CGACTGTGGA TATATGCTGG GGATCCCAAC ACAACGCAGC	300
TACTCTCGAG	310

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GAATTCCGGCC TTCATGGCCT AGTAAATATT TTCTTCTACT TTGTGTTTG CCTTTTTGTT	60
TTCTCAGCAT TATTTTTGAG ACACAAAAG ATTGATTTG AAGAAGTCTA ATTTATCAGG	120
TTTTTCTAG TAGTTTGTAG CGGATTNTG CATGCTGCTT TTAAAAAAAT CTTTGCTAAC	180
CCTCGAG	187

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GAATTCTAGA CCTGCCTCGA GCCTTGCCCA GAATCAGCAA GTAAACTGCA CTAATTGTC	60
TTATATTTGA CTTTCTAACCA CTGATTTTTC TGATTTTCC CTGTTGACC CTCCAATTAA	120
TAAAAATGTG TATAATTGTT CTGCTGCTTC TGCTTTGCC TGCTTTGGCT GCTGCATATA	180

CAGGTGAAGA TCTGGAAAGA AATGATGGAT CTACAGAAAA ACCCTACTTC GTAAACCCCTA	240
ACCTGCATGG AATTCTGATC AAGAAGCAAC TCGAG	275

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 287 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GAATTCGGCC TTCATGGCCT AGTTTCACAT TGTCTGTACT GTGTTGTGCA GTACCAGAAG	60
TTGCTGGTAG CTACTTGGTC TTCTGGGACC TGCCATTGCA GACGTGGTGA TTGTAATCTT	120
AATCTTGTG AAACAGGATG GATTTATGAC TGGGATGGCC GGAAGCCACA CCAGACACCC	180
AGTCACCTGG TCATGGGAGA GGTACTTTGT TGGCTTTCA TAGTACTTAA CACTGTGAGC	240
TGCTTCCTGA AGTGGCACTC TTAAGGCCAG GTGCCACAC CCTCGAG	287

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GAATTCGGCC TTCATGGCCT AAGACAGACA TTTTTGGCAG AGCATAGATG AAAATGGCAA	60
GTTCCCTGGC TTTCCTCTG CTCAACTTTC ATGTCCTCCCT CCTCTGGTC CAGCTGCTCA	120
CTCCTTGTC AGCTCAGTTT TCTGTGCTTG GACCCCTCTGG GCCCATCCTG GCCATGGTGG	180
GTGAAGACGC TGATCTGCCG TGTCACCTGT TCCCGACCAT GAGTGCAGAG ACCATGGAGC	240
TGAAGTGGGT AAGTTCCAGC CTAAGGCAGG TGGTGAATGT GTATGCAGAT GGAAAGGAAG	300
TGGAAGACCT CGAG	314

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GAATTCTGCCT TCATGGCCTA CACCAAGTTG AATCCCTATG CAGGAGGAGA CGGCCTTCAG	60
AACAAACCTGT CCCCAAGAC AAAGGGACT CCTGTGCACC TGGGCACCAT CGTGGGCATC	120
GTGCTGGCAG TCCTCCTCGT GGCGGCCATC ATCCTGGCTG GAATTACAT CAATGGCCAC	180
CCCACATCCC TCGAG	195

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

GAATTCTGGCC	TTCATGGCCT	ACACTCCTGG	TCATTTGCA	TTTTATCCAG	CTTTTTTCA	60
TCAACCATGT	TATCCTGACA	GACACATTA	TTGGATATT	AGTTGGAAAT	ACCTTATGGT	120
TGGTTGCACT	TGGCTATTAT	ATCTATGTA	CTTTCTGGG	ATACAGTGCA	TTGCCATT	180
TGAAAAATAC	AGTAATTCTT	CTGTATCCAT	TTGCACCTCT	GATTCTGCTC	AACTCGAG	238

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GAATTCTGGCC	TTCATGGCCT	AGGCTAACGT	AATTGAGAAA	ACCAAATGAA	ATATATCTG	60
ACCAATAATT	AAAACCATA	TCAGAGATTC	AGTTGGTTC	TGTCTCTGC	TTACTGATT	120
TTAGGATCAG	CCTCATACAA	AAGGGTAATG	GTGGCAGCAG	CTCCAGAACT	CATATCATAT	180
CCTCCCATGT	TAAAGTCAA	TGAGAAAAGT	CTGTCTCGC	CCCAGGATCT	CGAG	234

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GAATTCTGGCC	TTCATGGCCT	ACTCAGTTCC	ATTGTTAACG	AAGGAAAAAC	AAACAATACA	60
TTGAATTGAA	CAACCCACTG	AAGTTGCAGA	TAATGAGGAC	TTACCATTTG	ATACCATTAT	120
TCATCTGGAC	CTATATGTT	CATACAGTTG	ACACCATCCT	ATTACAAGAA	AAACCTAAC	180
GTATTATTATC	AAGCAAAAG	ATAGTGGTC	TGACAAAAGA	TGACGGTAAA	ATGCTACGTC	240
ACACCCCTCGA	G					251

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GAATTGGGCC TTCATGGCCT AAACCACTGC GCACCATATT TCTTAAGGAT GTTCTGAAGA	60
CCCATGAATG TCTGGTCAAG TCTGCTGATC TCTTAATGAG GGACACCTG TTTGAAATAA	120
TAACAAGCTC CAGGACATTC TACGTACAGG CAGACAGTCC AGAAGACATG CACAGCTGGA	180
TTAAGGAGAT TGGCGCAGCT GTCCAGGCCA TCAAGTGCCA CTAGGCCATG AAGGCCGAA	239

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

GAAAACCCCA GATATTCCCTT ATTATGGAAG AAGAACGAG AAATATGTTT TTGAATAATG	60
TGGGTCAAGAG AATTGTGCAT TTATTATTGC TAGGATGCAT ATACACATTG AACTCAGTCA	120
ACTTACTCTC TCTAAATTAT CTCACCGGTG GAGACATTGC CTCAGGAGTC GAGCCCTGTG	180
GTGTGCTCTCC TGCTGTCACC ACATTGACC ACCTAACTGA CCCCACTGTG GTCACCTTIG	240
CCACCAATCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GAATTGGGCC TTGCCAGTAT TCATGCTGTT GCTTCAGTCA AGAATGAATT CCTCAGCGCT	60
ACCTCTCTTG ACCTTCACAT CTTACTTAGT GCAAATGCTG TCTCCTCCTG AGACTTGCCT	120
GACTCGGAT ACTCTCCCTG TGACATCTTA TCTAAAATGT CAAGTGAGAC TCGAG	175

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

GAATTGGGCC TTCATGGCCT AAGTGGCTGT GTGGTATTTT CTAAGTATTT TTAAAATTTT	60
TCTCTCATTG ATACCCCTATA AAAATGCAAC TGTTAAAGAA TTTGTCTTTC TTTCTCATTA	120
TATTCTTCC AGAGTATATA ACTAATTAT TCAGCATTC A TTCAATTCA CAGACAGC AGATATTGT	180
TGAGCACTAA CTATGTTCA GCACTGGCA GGGATATCGG GATACCAAGA AAGCTCGAG	239

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 236 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GAATTCCGCC TTCATGGCCT AGAAAATAAT TTAGAGAAAG AATAGAAAAGT CATGGAAAAT	60
CTCATAGGTA GGAGACAGAA GAGAGAACAT TGTAAAATAAG TTTAAAAAAAG ATAAGAAAAT	120
CAGGATAAAAG TAGTATGGAC TCTGAGGTGG GAGAGAATT TAAGATTAGC AGGAAAAGTAG	180
TGTAGTTGGT ACTTTTTAGT TATTAACAAA GCACACTT CTTACAGAGT CTCGAG	236

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GAATTCCGCC TTCATGGCCT ACGAAGATTA TAATGTATTT TTATTCCTGTT TTCAGCTTC	60
TGTTTCCTGT TGCAGGTGGG ATAAGACCCC CTCAGGCCT GATGCCGATG CAGCAACAAG	120
GATTTCCTAT GGCTCTCTGTC ATGCAGCCTA ATATGCAAGG CATTATGGGA ATGAATTACA	180
GCTCTCAGAT GTCCCAAGGA CCTATTGCTA TGCAAGCCAGG AATACCAATG GGACCAAATGC	240
CAGCAGCGGG AATGCCTTAC CTAGGACAAG CACCCCTCCT GGGCATGCGT CCTCCAGGCC	300
CACAGTACAC TCCAGACATG CAGAAGCAGT TTGCGGAAGA GCAGCAGAAA CGATTTGAAC	360
AGCAGCAAAA ACTCTTAGAA GAAGAAAGAA AAAGACGCCA GTATCTCGAG	410

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GAATTCCGCC TTCATGGCCT ACACATTTGC ATTGTCTGCC CATGGACTGG TTGGAGCAGA	60
AACCTCCATA CCTCAGTCCTC TTGGTATTG TCTGCCCAA CTGCTGCTTT TTGTTGGGAT	120
GTGTTGTGT GCTGGGGTCT CGGCAGCATC GGCTGCTTC CGGTGCGCAC TGACATGCAC	180
TTGTTCTCCA CGATGGCTTT CTCTACCTTC TGAGATGCTC CATTATCAGT CCTGCCTTIG	240
TTCCGGAGAG TTGAGATGGT ATCACTTCTC ATCCATCCTT AGAAATACCC CTCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

GAATTCTGGCC	TTCATGGCCT	AGGGGGCTGG	TAGTGAAATA	TTGGTACTG	AAAGTGTGAA	60
GACCTCTGCT	GGGGACTGAA	CAGAGGGAGT	GTCTTCTGCT	GGTGGTGTGA	AATCTATCTC	120
ATCATCAAAA	TTATCTTCAA	ATTCCTTAAA	GTCTATTCT	GGGTCTTAC	ACGAGGATAC	180
ACAGTTGCA	ATTAACACTA	TTAATATTAT	TAAACTGCAC	ACACACAGGA	TCACAAAAGA	240
TGAGGAAACT	TCTGCAGCAG	GTGGCGCTCG	AG			272

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

GAATTCTGGCC	TTCATGGCCT	ACTACTTATC	ATCCCTGCTC	ACACACCCCT	GTCCAAGGCT	60
TTATGCATCG	GATTTATTTT	TCCAAATCAA	GAGGACAGTG	ATAGATGCAT	TTTCCCCAGG	120
CTGCTCTAGA	AAGGTCGCTA	AATGTATACT	GTGTCAGAA	TTGCTGAGAT	CTCCCCCCAC	180
TTTTGGTTTT	TGCAGCAGTA	AAAACTCTTT	CCACTGTGAC	TTATTTCTC	TCTCAGGCAG	240
CAGACTCGAG						250

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

GAATTCTGGCC	TTCATGGCCT	AGATCTTCTC	CCCATTCAAG	AAAACCTTCC	CATTCCGGTT	60
AATGGTTTTG	ACAAGCAGGG	CACCACGGGG	CATAAAATTG	TATCATCCAG	CCTCCTTCCA	120
GCAGCTCTCT	CCAGTTCTTG	TCTGTGATGA	TGGTACGTT	GCTCTGCCGC	CTGTGGGTCC	180
AGGGAGCACC	CCAAAGCAAC	AGTACCAAGGA	CTGCCACCGG	AACTGCAAGA	CTCCCTGGAGG	240
GTGCCATGTC	TGCCACTTGC	CCACCTCACA	GCAAGCGTGG	CGGCCCAACA	CTAGGTTTTT	300
TAAAAACTGT	GACTATCAGT	GTTTTAAAAA	TTGCCCGGTA	ACTCTAGACT	TCAAAAGTGG	360
GATAAGTAAT	GATAAACCAA	TAATAAACCC	TGCCTCGAG			399

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 185 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GAATTGGCC	AAAGAGGCCT	AAAAATTAAT	ATTACCTTAT	GAATGCCTT	ATCATGACTC	60
TCTTAGTGGG	GATTTCTGTC	CTCCACATGC	CCTGGGGGAT	GTGCAGCCCC	CGTGCACCTCC	120
CCGCCTTGGC	CGGCCCTTC	CCCCATGCC	AGGTAGACTC	TGAGCTCTTA	GCCCCAGCAAC	180
TCGAG						185

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAATTGGCC	AAAGAGGCCT	AGGAACTAA	TCTTAAACAC	TGAACCTCTT	TTCAGCAAAT	60
TGGCTTTCTA	GTTCCTCAGC	TCTCTCTTAA	CACCTCTAAA	TCTCTTCCT	GGCAAGATCA	120
TTTATTTGCC	TTGGTTTATG	GTGATACTCT	TCATTGTTAT	ACTGGTGGGT	GATTGTTTTA	180
ATTCATAGCT	CTTTTTTCT	ACTTCAAGGAA	GATGACACTG	CTGGCTCTGC	TGGCTCTGAT	240
GTTCACCTTG	TGGCTAATGC	CTGTTTGC	CTGTGTTCAC	ATTTATTCCA	CGATTCACTT	300
GTAAACATTT	ACTAAGCTCG	AG				322

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

GAATTGGCC	AAAGAGGCCT	ACTCATAACA	GCGTCAGAGA	GAAAGAACTG	ACTGAAACGT	60
TTGAGATGAA	AAAAGTTCTC	CTCCGTATCA	CAGCCATCTT	GGCAGTGGCT	GTTGGTTTCC	120
CAGTCTCTCA	AGACCAGGAA	CGAGAAAAAA	GAAGTATCG	TGACAGCGAT	GAATTAGCTT	180
CAGGGTTTTT	TGTGTTCCCT	TACCCATATC	CATITCGCCC	ACTTCCACCA	ATTCCATTTC	240
CAAGATTTC	ATGGTTTACA	CGTAATTTC	CTATTCCAAT	ACCTGAATCT	GCCCCCTACAA	300
CTCCCCACCT	CGAG					314

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

GAATTGGGCC AAAGAGGCCT ATTATGCTGG TGCTGCTAC TAATTCAGG AAAAAGTACA	60
AGTCTGGCTA GACTCTGCTA CCGCCTAGCA CTGAGGTGTG GTCCCTTATC TGTTATTACA	120
TTCTTCTGTA TAATGAAATT CTGAAACACA TGCTCCAGGC ACCTTTGTAATGTGAAGGT	180
GAATAAAAGTA TTGTTTGTT GTCTGAAAAG AGATCTTGA AATGTTAAGT TGCCACAGAC	240
CCAGACCAAG GAGCCTGCTG AGAGTTTAA AGGCTCTTAT TGGATGACAG TAGATTCTT	300
CCTGAAATG TCTATAATGA ATATTCAAGA ATGCTCATTG TGATGAAAT TTGCAATT	360
AATTATCAGT GAAAGAAAAG ATTACACAGT GCTAAATGAT TGCCATGGAA AAGTTATGGC	420
TACCTCTTGG AGTAGAGAAA ATCTCAAAGG CCGCTACTCG AG	462

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

GAATTGGGCC AAAGAGGCCT AGTGGGCAAC TTGGAGAAGA GTGAAAAACA CTAAAGAATC	60
ATCTCTTTTC CGAGTCACAA AGTCCCAGTA ACTTTGTGAC TCAGAGACAC TTTTCGTGAA	120
AATTACCTTT CGCGGGGACA CCGTCTCAGG GCAGCTTTT CAAGGCTTCG CTTGACATGA	180
TTTCCTTCTC TTTCATCAGTC ACTTTGGATC CAGCTGAATA TCTCTCTCGG GTGAGAGCGG	240
ATGTGGACTG GCCTCCCACA GAAGAAGAGT AGGTGGTTT GGTGGGGGTT GGGGTGCGGG	300
CTGGCTTCCT GGTCTCGAG	319

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

GAATTGGGCC AAAGAGGCCT AGTGAAGAAGA AAGAGACTGT NAAATAATTG TGCAATATCCT	60
CAGTGGATAA TTCTGTNACC TATCTGTCAG CTATTCATA TCAATAAAAGG ACACAGCTGG	120
TAATCCAAAA GGAAAGGATC TCTTGATGAA AGTGTCTGC CATTCTTATT AAAGTCAACA	180
TACAAGATAC ACTCTTAGTG ATTTTGAAAC CCATAATTAT ATTGTCGTA TAATAATTGG	240
CACTTAACGG TTACAGAACCA CTTTCACTGA TATTTCCCTT AGTGAATCTT ACAAACAAATT	300
CTACCACTAA TTTCATAATAT TTGCCATGAT TAGACTTCA AAATTAGTCC ACGCACTCGA	360
G	361

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAATTGGCC	AAAGAGGCCT	AAGAACATG	GCGGCCGCA	CGTTGACTTC	GAAATTGTAC	60
TCCCTGCTGT	TCCGCAGGAC	CTCCACCTTC	GCCCTCACCA	TCATCGTGGG	CGTCATGTTTC	120
TTCGAGCGCG	CCTTCGATCA	AGGGCGGAC	GCTATCTACG	ACCACATCAA	CGAGGGGAAG	180
CTGTGAAAC	ACATCAAGCA	CAAGTATGAG	AACAAGTAGT	TCCTTGGAGG	CCCCCATCCA	240
GGCCAGAAGG	ACCAAGTCCA	CCCAGCAGCT	GTTCGCCAG	AGCTGGAGCC	TCAGCTTGAA	300
GATGATGCTC	AAGGTACTCT	TCATGGACCA	CCATTGCTG	TTGGCAAGAA	ACGGCTTTAC	360
TTACAAAACA	GTCTCGAG					378

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAATTGGCC	AAAGAGGCCT	ACTCTGAATT	AATGCAAATT	CCCGTTGTAC	TGTATTTAAT	60
TATGCACAAA	ATGGTGCCT	TGACTCGAT	TTCAGTGAAG	AACTTCATTT	TTTTACTTTT	120
AAAGTCTCCAA	GTAGGAAATT	CAATTAGCGT	TATGAAAGAA	ACACTAAAAC	TCGAG	175

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

GAATTGGCC	AAAGAGGCCT	AGGCAGCAAT	GTATCTGTC	CTTCATTCTT	GCATGTTTT	60
GGAAATTGCT	TTTGCTTTA	CTTTGGTCG	TCATGGCAAT	CACGTGCCCT	CTCTGGTTCA	120
TTTTGACACAG	ACCTGCCTAG	AGCTGGAACG	TTACCTCCAG	ACCGAGCCCT	GCTATGTTTC	180
AGCCTCAGAA	ATCAAATTG	ACAGCCAGGA	AGATCTGTGG	ACAAAATCA	TTCTGGCTCG	240
GGAGAAAAAG	GAGGAATCCG	AACTGAAGAT	ATCTTCCAGT	CCTCCAGAGG	ACACTCTCAT	300
CAGCCCGAGC	TTTTGTTACA	ACTTAGAGAC	CAACAGCCTG	AACTCAGATG	TCAGCAGCGA	360
ATCCTCTGAC	AGCTCCGAGG	AACTTTCTCC	CACGGCCAAG	TTTACCTCCG	ACCCCATTTG	420
CGAAGTTTG	GTTCAGCTCGG	AAAAATTGAG	CTCCTCTGTC	ACCTCCACGC	CTCCATCTTC	480
TCCGGAATG	AGCAGGGAAC	CTTCTCAACT	GTGGGGTTGC	GTGCCCCGGG	AGCTGCCCTC	540
GCCAGGGAAAG	GTGCGCAGCG	GGACTTCGGG	GAAGCCAGGT	GACAAGGGAA	ATGGCGATGC	600
CTCCCCCGAC	GGCAGGGAGGA	GGGTGCACCG	GTGCCACTTT	AACGGCTGCA	GGAAAGTTTA	660
CACCAAAAGC	TCCCACCTGA	AAGCACACCA	ACGGCTCGAG			700

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAATTGGCC	AAAGAGGCCT	AGAAAAATAC	TTGGGCAGAA	AGAAAATATC	ATCAAATAAC	60
ACCTATTTCT	TTTCAGCTAT	AGAGATGGCT	GGATATCAA	AGCACCCACCG	GAGCTTTCGA	120
ATTTGCTGCC	TCTTTTCAGC	CCTCAGCTTG	ACTCTCACTT	TTCAAGAGGG	AGAAAATGAA	180
TGTTTCCCAG	CATTCTCTGT	CCTTGTCTCC	AAAGAAGAGA	GCAGGTGTTG	GCTTCCAAAC	240
CTTCCGTATT	TTCTTATTGC	TGTTAGGGGG	ATCAACTGCA	TGTTCCCTGA	GGGAAAAGGG	300
TGGCTCACTG	ACCTACTTGA	AGGCATTCTC	TCAGTGGAAAG	CTGGGCAAGA	GAATCCAGGG	360
ATTTCTTTG	CAGGTTCTG	CGCAGTGCC	CTGCCATCAA	GCTGCCTAAA	ATGTGAATAT	420
TGCTTCCCTG	CGTTTCAGAG	GTGGCCGCTC	GAG			453

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

GAATTGGCC	AAAGAGGCCT	ACAAAATGTG	AATGGAACAA	ACCTGCACGT	GTACCCCTGG	60
ATGTGTGGAT	GTTCCTTGT	TTTATTTGTT	AAACCTGATG	TCTTGTCTGT	ATGACACATT	120
TATGGAAAC	GTTCCTTCCC	TATTCCTGTT	CTTGTATTT	ATTTTCTCGT	GTTCCTCCAA	180
GAGCAGATAT	TTTAAATTT	TATATAAAC	CAGTTCTCA	ACATTTTAA	AGGGTTCATG	240
CTTTTTGTAT	CCTATTTCA	AAAACTTGG	CTACTTCAG	GTCACAAAGA	TTTTGGATT	300
GTTTTAAATCT	ACAGTTTTA	TAGCTTGAC	TTTTATATAT	AAGTCTGATT	CATTGGAGT	360
TAATTTTGT	GTACAGTGT	AATTAAGGGT	CTAGGTTCAT	TTATTTCTT	ATGAATATCC	420
AATGGTCCT	CGAG					434

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GAATTGGCC	AAAGAGGCCT	ACAAACACAG	AACTTCCA	TCGTTGCAGA	GAGTACTATT	60
AGAGAGCA	ATTCAGAGC	CTGTGATCTT	AATCACTACA	CCTAAAGCCT	CCCAGTTGAC	120
AAAGTTACCA	CTCTTTTTTG	GTGTGTGTG	ACGTGCGTGT	GTGTGTGTGT	AAGTATATAT	180
AATTTAAATC	ATTCATTA	ATTTACCTCT	GAAATTCAA	AGACTGAAAC	AGATCTTCTT	240
TTTATCAAAT	AAGTTGATTC	CAGAGATTAT	ATTGGTGT	ACATTCAGG	CAACCTGCTC	300
ATGAAATTAT	CCATTGCTCT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

GAATTGGGCC AAAGAGGCCT ACTCCTCCGC	CTGCAACCAT TGTTTCTAC CACTGGATTA	60
TTCTGAAGCA AATTTAGAC ATCATATATA	TTTATCTCTG AAAGAGGACT CTTAAAAACAA	120
TGCACTTATA CCTCTATTAC ACTGACAAA	TTGGTAACAA TTCCCTTATA TTATCAAATT	180
TCCATTGATG TGTCCTGATG TTCAAATTTC	TGATTCTCCA GATGCTCAA ACTTCCAGAA	240
ACACAGATTC CCAGATGGAA TCCTGGGAA GGCTCGAG		278

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

GAATTGGGCC AAAGAGGCCT ATTTCTAAT AAAAACTATT TTATGGTAGG TTTTGTGGAT		60
TATTGAATAC ATCTGGCAT TCTGTTAAT ATGTATGTT TCCTGAATGA GGGGGTACAT		120
TGTAATTATA ATTATTAAC TCACAATGTT TTGGTTTA AAAATAAAA TTTAGGAGC		180
AAGCAGTGTGTT CCTGCCTTCT TTTCTGAAGA TGATTCTCAA TCGAATGACT CAAGTGATTC		240
TGATAGCAGT AGTAGTCAGA GTGACGACAT AGAACAGGAG ACCTTTATGC TTGATGAGCC		300
ATTAGAAAAGA ACCACAAATA GCTCCCATGC CAATGGTGCT GCCCAAGCTC CCCGTTCAAT		360
GCAGCTGGCT GTCCGAACAA CCCAGCATCA GCGAGCAGCC AGTACAGCCC CTTCCAGTAC		420
ATCTACACCA GCAGCACTCC ACCTCGAG		448

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 187 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

GAATTGGGCC AAAGAGGCCT AACTTTGTGTA ATTTGAATTG GGTCCCGCTT AGTTCTTGAA		60
TTGTTATGAA AATCCTATAT CTGTTGTAT ATTTGCAAAC CCTTTGTATT ATAATTGTG		120
ATATTTTCCC TTTTAAAAAA ATACCATTGA AATCAGCATG ACAAAAATAA CACTGTGGGC		180
ACTCGAG		187

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 349 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GAATTCTGGCC	AAAGAGGCCT	AGACCAGAAT	AAGCCTTTA	AGGTAAACCT	CAAATTATC	60
ATTTTATGGT	AATACTGACC	ATTTTAGTCC	CCTAGTTTG	ACATGGGAGA	TAGTGACTAC	120
ACTGGTGTCT	GACTTTTTTC	CTAGAGATT	CTCCCTGAAA	AATACAAGGG	CTGTTGGTGA	180
GAGCAGACTT	GAGGTGATGA	TAGTTGCGCT	CTGGTCTACA	AAGATTTCAT	AACTCCTTGG	240
AAAGCTTCTT	ATAATCATTC	TTAACCTCTT	GGTAGCTAGA	AATTAGAGT	AGTTGAAATC	300
TTTAGGAATG	AACTTCTGAG	GGCCAAAAAA	TGTGACTGAC	ACACTCGAG		349

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

GAATTCTGGCC	TTCATGGCCT	ACATCACCAA	TCGGCTGGG	TAAGGGTCCC	CATGAAGGCG	60
CAGCGGGTA	TAGAGGTGCA	GGGGAGAGCA	GCCTGGGGAG	TCCCTATCTG	GATAGGCTCC	120
AGCCTGGTC	GGGGCGGTCC	TGGTGCCTGG	TGAAGCGTCA	AAAGAGGGAG	CCTGAGCGGG	180
GCAACGCAGA	AGGGTGGAGA	GGAGGGGGTG	GCGAGGGCGG	GCAGCGAGGC	CTGGAGCCGC	240
CAGGAGAGGG	GGGGGGGGCG	GCCCTTCTCC	AGGAATTTC	GGGGATCGTG	TTACAGCGTT	300
GGCGGAGCCC	GAGCGGAGTG	GGACTCGAG				329

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

GAATTCTGGCC	TTCATGGCCT	AGAAAGGGGA	GGGAACGTGA	CAGGCAGGTG	TGGGATAGGG	60
ACTTCTCTTC	CGGTCAAGAGC	AAGGGTCTC	CGAAACCAAA	ACAACCTCT	TCCCTTCATC	120
TCGCCCCGGA	TCCAAAGTCT	TGGGGCTAGG	CTGGGGCGGG	AGTGGCACGG	AGATGTAGGA	180
ACACTGCCTT	TCGTTACTTC	TCCIGCCATG	GCTGACCTT	TTGTCTCTTG	TTTCATGGTT	240
TTACACGTAT	GAATGGCTTG	AGACTGAGGA	TTTGGGAAG	AAGCGAAGGC	ATCATCTAGG	300
GCTGTGCTGT	GCCAAGTTGA	GCAGTTGTTT	AAACTGTTAG	AATTGGTAC	TGGTGTAAAA	360
ACCCCTCTATG	CTCGAG					376

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GAATTCTGGCC	TTCAAGGCCT	ACGTGAAACC	CCATCGGCTT	CATTGGCTCC	TTGATTTAAA	60
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CCACGGCCGG	CTNTCTGCC	TCTTGATGC	TGCTGGCCA	GGTTGCCAG	CCATATCCA	120
GCCCCGCTG	CAGGGAGCCG	GAGGCGCTG	CTGCTGCTAT	TGTGTGGATG	CCGGCGCTGT	180
CTTCTCTCT	TTCCAGAGAT	GGCTAACAGG	GGCCCGACCT	ATGGCTTAAG	CCGAGAGGTG	240
CACGAGAAGA	TCGAGCAGAA	GATCTCGAG				269

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

GAATTGGCC	TTCATGGCCT	AGATGTGTTG	AACCTTATT	TTGTACATT	ATTCAATCAA	60
GGCAAAC	TTT	TATAATT	TTT	CTT	CAATGAC	120
TATTCTATG	C	AACTATAG	TTT	ATAC	TTTGAC	180
ACTGGTTG	GAG				GTAT	197
					ACATTGATT	
					GCTCGAG	

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GAATTGGCC	TTCATGGCCT	AGCAAGAC	TTAAGTATA	TACTCTGAAA	GTGTGGCTAA	60
TATGATCATG	ATGCTGTAGG	AAAAAAAGGT	TATATGTCCA	AGTGTATGTA	CTTGAAATG	120
TGCCTAAAGA	AACCTGGAAG	GATA	CACAGG	TCTTCC	GGTACAAGAC	180
GATCATCATC	TAACTCTAC	TCTTCC	TTT	TACTCTCTG	GGAGAACTGG	240
TGTATACATG	GATTACTGTT	ACTTAGCAGG	GGGACCGGT	TGGCAAAGC	CTTGGTGTGC	300
CCTTGGCACA	ATTCTGCCAA	GACCC	TTAC	CTCTCC	CTCANGCTC	360
TCTCCCCACA	TCTGGAAAAC	CCTGGATACA	TTT	CTC	CCTTAACCCC	396

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

GAATTGGCC	TTCATGGCCT	AGGAAGAGGT	TGAGAAGACT	CCTGGGCTTC	AGCCTCTCCC	60
ACCCAGCCCT	GCCCCTCACC	TGCCTGCC	CCCCTCCCC	ACTCTATACT	AGGGACTGG	120
TCTCAGCTC	TGATCAGTTT	CACAAAGTTT	GTTCCTTAAG	GAAATCAAAT	CCCATTGTCA	180
CCTAACTCTG	AAGATCTAAA	TAGCCCTTGG	ATCAGTACGG	GAACCCAAA	TCCCCACAGGG	240
CCAGATGTGG	AGTCTGTGTC	TGCCCCCGTC	TTCTCTCCAT	CCTCAAAGCC	CCCACTTCTC	300

TCCAGGCTGC TTCTCGAG

318

(2) INFORMATION FOR SEQ ID NO:207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GAATTCTAGA	TCTGCCCTC	GGAAACAATGG	GAATCGGC	GC	GGAGGTGCT	TGGGCCGCG	60
TGCTCCCTGG	GACGCTGCA	G	TGCTAGCGC	TG	GGGGGC	AGCCAGCCA	120
TGGCCGCATC	TGCAAACATA	GAGAATTCTG	GGCTTCAC	CAACTCCAGT	GCTAACTCAA	180	
CAGAGACTCT	CCAACATGTG	CCTTCTGACC	ATACAAATGA	AACTTCCAAC	AGTACTGTGA	240	
AACCAACCAAC	TTCAGTTGCC	TCAGACTCCA	CTAATACAAC	GGTCACCACC	CTCGAG	296	

(2) INFORMATION FOR SEQ ID NO:208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

GAATTCGGCC	TTCATGGCCT	AGTCTCTTGA	AAAGCCGCAT	TTCCAGGCGC	TTGGCCAGTG	60
GCCTGGGAAG	TAGCCTGTG	TTGTATTGAG	ACAGTCCCC	AGCACAAAC	CATGTTCCAG	120
TCATTCCTT	TCCTACTTTG	GGGATTGTTG	CCTTTCTGC	TTGTTAAAG	TAAAACAAGC	180
ATGTACTTGT	TTGTATGTAT	GTATGTATGT	AGTTGTACGG	TGGCACAAA	AAAAAGAGG	240
GCTGTATCCA	AATAAAATCAT	TTCTGGCTGC	TCACTGGCAC	AGTCCCTTG	CTCCGTCCCC	300
TCCTGGCTCG	AG					312

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GAATTCGGCC	TTCATGGCCT	AGGCAGCGTT	TCACCGCTGT	GGAGGACCA	TATTACTGCG	60
TGGATTGCTA	CAAGAAC	TTT	GTGGCCAAGA	AGTGTGCTGG	ATGCAAGAAC	120
GGAAAAGGAC	TGTGTCAAGA	GTGAGGCCACC	CAGTCTCTAA	AGCTAGGAAG	CCCCCAGTGT	180
GCCACGGGAA	ACGCITGCC	CTCACCC	TTCCAGGCGC	CAACCTCCGG	GGCAGGCATC	240
CGGGTGGAGA	GAGGA	TTGT	GGTGTCT	TTATAGAAAA	AATCGAAGCT	300
TAGCAGCTCC	TCGAG					315

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GAATTGGCC	AAAGAGGCCT	AGGAAGATGG	CGAAGGTCTC	AGAGCTTAC	GATGTCAC	TT	60
GGGAAGAAAT	GAGAGATAAA	ATGAGAAAAT	GGAGAGAAGA	AAACTCAAGA	AATAGTGAGC		120
AAATTGTGGA	AGTTGGAGAA	GAATTAATT	ATGAATATGC	TTCTAAGCTG	GGAGATGATA		180
TTTGGATCAT	ATATGAACAG	GTGATGATTG	CAGCACTAGA	CTATGGTCGG	GATGACTTGG		240
CATTGTTTG	TCTTCAAGAG	CTGAGAAGAC	AGTTCCCTGG	CACTCACAGA	GTCAAGCGAT		300
TAACAGGCAT	GAGATTGAA	GCCATGGAAA	GATATGATGA	TGCTATACAG	CTATATGATA		360
GGATTTTACA	AGAAGATCCA	ACTAACACTG	CTGCAAGAAA	GCGTAAGATT	GCCATTGAA		420
AAGCCCAGG	GAAAAATGTG	GAGGCCATT	GGGAGCTGAA	TGAGTATCTG	GAACAATTG		480
TTGGAGACCA	AGAAGCTGG	CATGAAC	TTG	CACTCGAG			518

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

GAATTGGCC	AAAGAGGCCT	AATTGAATT	CATTTCTTT	GTAGACTAAT	GTTACAATAA	TT	60
ATAAAATGGGA	ATTTAAATA	CCTGCATGTT	CTGTTTTCT	CTTTTTCTT	TTTCAGCCA		120
TAATGAAAGG	AAAGTGACCT	GCAAACATCC	AGTCACAGGA	CAACCATCAC	AGGACAATTG		180
TATTTTGTA	GTGAATGAAC	AGACTGTTGC	AACCATGACA	TCTGAAGAAA	AGAAGGAACG		240
GCCAATAAGT	ATGATAAAATG	AAGCTTCTAA	CTATAACGTG	ACTTCAGATT	ATGCAGTGCA		300
TCCAATGAGC	CCTGTAGGCA	GAAC	TTCAAG	AGCTTCAAA	AAAGTTCAT	ATTTGGAAA	360
GAGGTCAAAT	TCATTAAAAA	GGAA	TCTAA	TGCACCGGC	GATCTCGAG		409

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 411 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

GAATTGGCC	AAAGAGGCCT	AGTACAGTCC	CAATCAAGAA	GCCTTATTAA	CCTTCTGTGT	TT	60
GAGGGACTAG	ACTCAGTGT	GGGTTTGAG	GATCCACTGG	TGAGGAGCAT	TCAGTCTAGC		120
AGGAGAAAATG	TCAGCATTAT	TTATTACACA	ACAAGATCTG	ATGCATTCTAG	ATGACTTAC		180
AGGTCTAGGA	ACTGTTCTAGA	GGAGCACAAA	TGAATGAGAG	AGAGAGGGAG	AGAGGGAGAT		240
TGAGTGAGTT	AGAGAGTTGT	TGGTGCTCCA	CAAGGAGCAG	TAAAGTATT	TAAAATAAA		300
AAATAATAAG	GCTGACTCTG	TGTCTGGCT	AGGGGTTGGC	CATGCTCCAC	AAAAAGCAGT		360
AAAGTGTTT	TGTTTTTGTT	TCGTTTTTT	TTTAAAGACA	GACGTCTCGA	G		411

(2) INFORMATION FOR SEQ ID NO:213:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

GAATTCTGCC	AAAGAGGCCT	AGTTTNTACT	TCTTACCTAT	TTACTGAATG	CNACATTACT	60
GCACACCAAG	ACAAAAGAGC	TCTCCAGGAA	AAACATTGGAT	ATATTGAGAG	CATTAAAAGA	120
TACTGCAAA	GCTCTAATAA	ATTCAGTCTG	CTTATTTTCC	AAATTTCTATA	AACTACATAC	180
TTAGGAAACT	GTGCTTTCAG	TGAGCTAAAC	TTCTTTTTT	AAGTAACATAT	CATAGTTTA	240
AGAAAAACAT	TTTAAAGAAGA	CAAAAAGTAT	TTATTAAGCC	CATCTAAAAG	GCTAATGCAA	300
ATCCCCAAA	AAGGAGCACA	TAGAGATAGG	CATCTCGAG			339

(2) INFORMATION FOR SEQ ID NO:214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

GAATTGGCC	AAAGAGGCCT	ATTGAATTCT	AGACCTGCCT	CGAGACACTA	GCCCTTTTTT	60
CTGTTGGTTT	AGCACAAATA	CTTCCCTCCT	CCGGCACCTC	CAAACCTACC	CCACAGTCAG	120
TGTACTTGT	TTATATATAT	TTAACCTTAT	TCAATGGAAA	CCATGCTTTT	GTCGTTTAT	180
ACTTTGCTAG	GTAGACTTCT	CGAG				204

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

CTCGAGAGGC	GCATCTTCAC	TGGCATATGA	CAGGCTGTCA	CTGCAGCTAA	TGTTGGTACA	60
GTTCCTTCAA	AGACCTACTG	ATGCATCTAC	CGTATTGGAA	ACCAACCGAGA	CATTGGCAAT	120
GGTGCTAAC	AATAGCATAA	TAACAGTAGC	GATGTGGACC	ACAAAGATAC	CAGCCACCAA	180
TACCAACATG	TGGCTCTT	TTTTTTGTT	AACTTGTGAG	CAAAGAGAGT	TCTGAAGGGT	240
CCCAGCGACA	GAGGCACCTCG	AGGCAGGTCT	AGAATTCAAT	TAGGCCTCTT	TGGCCGAATT	300
C						301

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

GAATTGGCC	AAAGAGGCCT	AAAATATTTG	AGTCTAACT	TATAAATTT	GCATTCTCCC	60
TAACGAAAAA	ATTCTATTA	CTGTTGGA	TTTCTTAA	TTTGAAATAT	AGTTACTGAA	120
ATATTAATTC	TTCAATTAA	ATTTATATT	ACTCACTGGT	TCCTTCCCT	TCTTTAAGGA	180
GACAGAAAAC	ATTAACACTT	TTTAACCTCT	CATTTGTTA	AAAATTTATT	GACCTCTCCT	240
CTGAGACAGT	TTGTATTCCCT	AGATCTCTT	AAACATAAAAT	ATGCTTATTT	TCAAGTTTTT	300
GTCACAGTAT	TCACTCGAG					319

(2) INFORMATION FOR SEQ ID NO:217:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GAATTGGCC	AANGAGGCCT	ATTTAGATTT	AACCCAGTTT	GTAGACATTT	GCATAGATCA	60
AGCAAAACTA	GAAGAGTTTG	AAGAGAAAGC	ATCAGAACTT	TACAAGAAAT	TTGAAAAAGA	120
GTTTACCGAC	CACCAAGAAA	CTCAGGCTGA	ATTGCGAGAA	AAAGAGGCAA	AGATTAATGA	180
GCTTCAAGCA	GAGCTACAAG	CTTTAACGTC	TCAGTTGGT	GCCTTGCAG	CTGATTGAA	240
TATTCCCTTG	CCTCCCTCTA	AAGAAGGTGG	AACTCGAG			278

(2) INFORMATION FOR SEQ ID NO:218:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

GAATTGGCC	AAAGAGGCCT	ACCTGGCTCA	TTTATAACCT	CCTCGATCCT	ATTACTGATT	60
TGCATTCTTA	ACTACAGGTA	AGAGAAAACC	AGTGCAACCT	AGCTTTCAT	AGACAGGAAT	120
TTGCTGGCTC	ATATAAATGA	GACATCCAAT	AAAGAAGAAA	AGTTGGAAAA	AATGTGTCAA	180
ATGTAGCATC	CTCTCTCTCT	CTTTCTCTCT	CTCTCTGTTT	TTTCACCTAG	GCTTGTGCCA	240
TAAACCTGCT	TCTCATCAG	TTACTGTGGT	TATGGCGTC	TTGTTGGCTG	AGCTCGAG	298

(2) INFORMATION FOR SEQ ID NO:219:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

GAATTGGGCC	AAAGAGGCCT	ACTTAGCAGA	ATATATTCTT	TAATAGCTCC	CATAAAGCAA	60
ACAAACCAA	AATATATTCT	CCTGACCCCA	CATTCACTTC	CAACTATCAC	CCTACATCTA	120
CATTCTCCCT	TTCATACCAA	ACTTTTCCA	AGCAGTTGTC	TATATTATG	TCTCCACTTC	180
TTTACCTCCT	ATTCTTGCTT	CAGTATGCTT	CAGTTGAGCT	TCGTCACCCCT	GTAGTCCACC	240
ACCAACTCGA	G					251

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GAATTGGGCC	AAAGAGGCCT	AGATTGATTC	TGTGTTGTGG	TATTGGCCCT	TACATACAAAC	60
TGGAGGAAGT	GTGAATTTC	TCATGTTGAT	AAATGGACT	GTCAATGATTC	TTTATAATTA	120
CTTCAATGCC	ATGTTTGTG	GTCCGGGCTT	TGTCCTCTG	GGGTGGAAAC	CGATGTGTGA	180
TGAAGATGGA	CCATCACTGT	CCTTGGATCA	ACAACTGTTG	TGGTTACCAA	AATCATGCTT	240
CGTTCACACT	GTTCCTCCCTT	TTAGCACCAC	TGGGTTGTAT	CCATGCTGCT	TTCATTTTG	300
TGATGACTAT	GTACACACAG	CTTATCATC	GGCTCTCCCTT	TGGGTGGAAC	ACAGTGAAGA	360
TCGACATGAG	TGCAGCACCC	TCGAG				385

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

GAATTGGGCC	AAAGAGGCNT	ACCCNGATTA	TAGTTTTGT	ATTGTTTTA	CAATTTTTGT	60
GAATTAGGAT	CCAAATAAGG	TCTGAAATA	TTACATTGGG	TTTAGGTAAT	CGATACCTTT	120
TTTCTTTAA	TCTATAAGT	TTCCCTATC	TTTTTATTGT	CGTTATTCCC	ATACAATTGG	180
TTTGTGAAAG	AAGCCAGGT	TTGCCCTAT	AATACTTCTC	AGAATCTAGA	TTGTGTTGAT	240
GAGATCCCAG	TGGTTTCATG	TAATATGTC	TTTGTCCCT	TGTATTCT	GTAAATTTG	300
TTTATTTAT	TTTTTTATT	TCTATTATTT	GAGATGGAGT	CTTGCAGTGT	CACCCAGGCT	360
AGAGTACAGT	GGCATGATCT	CAACTCACCG	CAACCTCGAG			400

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 481 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

GAATTGGCC	AAAGAGGCCT	AAGAGCCTAT	AAGGTTTACA	TATTTCACTG	GAGAGAGAAA	60
TAGGGACATA	CAATAAATGA	TTTTATAATA	AATTTCCATG	AAAAGTGAAT	CTGAAAACCC	120
CACCGGAAGG	CAGAGTAGTG	CAGCCAAAGG	AGCATGAATT	GTGGAATCAT	ACAGCTCTAG	180
GTTTCAGATCC	TACCTTTACC	ACTTGATAGC	TAGGCAGACT	TCAACAACTT	AGTCTAATT	240
GAGCTTCAGT	TCTCTCATCT	GTGAAAAAGA	GAAAATACAG	CCACTTTATA	ACATTATT	300
AGATGCCATA	AGGTAGGTAA	AGTGCCAGAC	ACATAGATT	AAAATCTCA	ATAAAATAGG	360
AAGGCTGGAA	TTTCCAAAT	TTTTCTTGC	TTTCACAATC	TGGTTCTAA	ATTTATTATT	420
ACTCTACCCA	TCACTTCCTC	CTTCTCCCTC	CACAACCTCA	CTATAAGCCC	ACATCTCGA	480
G						481

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

GAATTGGCC	AAAGAGGCCT	AGTGTCTGT	AGAGGTCTCA	GCATTTCTCT	TAGTATTGAA	60
CTGTATTAGT	TTTACATATT	TCTTCTTTG	TTTAGAGTAT	AACCGCTTCT	TACATTTCC	120
TCAGTCGTTT	TCTAAAGAAG	AAATTAATCT	TTTAGAAAT	CCTGGCAGTT	ACCCCGCAAT	180
TGATGTTTG	GTGAAAATT	AGAGCACACC	AGTTTGTCAT	AACTTTAAGA	AACATTTCA	240
CTTTATTGAT	ATTCTGAGGA	TTTTAGTGAT	TTGGGTTAATT	TGGGTCTAAT	AAAGAGTAAA	300
TGTTGAATA	CTCATTTGTT	TTGAGTCATC	TATATTTTA	AACCTTTCT	TTAGTTGTTT	360
TTTCATCCCT	AATAACAAATG	CAACTTTCCC	ACTTGCTCGA	G		401

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 465 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

GAATTGGCC	AAAGAGGCCT	AAACTGATGT	CTTCCATTG	CTGGATAGGA	CATGCTGACT	60
GATGACCTCA	CAGACTGTT	TTATGCCCTC	ACTACTCACC	TCACCACCTA	CAGTCATAGG	120
CTGACTAGGA	GTGGTTGTG	TACATTCTA	AACCTTTTG	CCCTTTTAT	TTGTCTTCT	180
AAGTGTGTAT	TCAGTACTAT	GTAAATTGAT	AAAACATGAG	TGTGAAATA	TTTTTTTTG	240
CTATAAAAT	GTAAATTGAA	TTCTTTGGG	AAGAGCTGAT	AAAATATGTC	ACTTAAAGAT	300
CTTGTAAAT	TAGATGAGGG	AGATATAGAT	GACAGAACT	CTTCAACAA	ATATCTAAA	360
AGATGTGCCA	CTCCAATTAT	TTTGTGAGTG	TCTTCAAGTT	TGTCCCCAC	TTTAAAGAAA	420
ACCAAACCTGG	CCATCATAGC	CAATGAATTA	TGCAGGAGTC	TCGAG		465

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

GAATTCTGGCC	AAAGAGGCCT	ACACATTATA	TTAGATTCA	TAGAAACTGT	TGGAAATATC	60
TAGCACATGT	GCTTTATCCC	ACAATAATT	CATAGAAAAT	TAAAAAGAAT	TAATTCTAAT	120
GTAACCACATCT	TTTTACTTGA	CTTTTTTTT	TTTGCTCTG	CTCACAGGTC	TAATTGTTGT	180
TATTCTCACT	TTATTTTCT	ATAAGGTAGG	AATAATATCC	ACTTCATTAG	CTCATCATGA	240
GGGATAAGTA	GGATTGGAAA	AGATACTTTC	AAAGGGCACC	TAACTGTGAA	GAAGATGCCT	300
TCATTGCA	TTCTTTCTG	GCACATTCT	TGTTATCCAG	TCATTCATTA	GGACTCCATG	360
TTTATTGAAC	ACTACTCTG	TGCCAGGCAC	TTTTCTCTGT	TCTGAAATA	TCACCATGTA	420
AAAACAAATA	GCTGAAGAAT	GCCCTGCCCT	CATAGAGCTT	ACAGACATAG	AGCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

GAATTCTGGCC	AAAGAGGCCT	AGCGTTCTG	ACTTTATTAC	TGGTAATT	TTGCACAGGT	60
TTTCTGCAT	CAAAAAAGTA	TCTGCTAAA	TAGAGAAAGT	TGTGCTGAA	TTCACATTTC	120
CCCCCAACTT	CTAAAAAATAT	TTCCCTAAA	AAAGAATCCA	CTCATCTAAT	TTTAAAGAAA	180
ATATACTTCT	TACACAAGAC	AATCCAAACT	GATGCAAAT	ATTTATTCCA	AGTTAGTTAT	240
TTTATGCAGT	AGTTTCCCCC	TCGAG				265

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

GAATTCTGGCC	AAAGAGAGAA	ATTTTAATCT	TGAAAGACTT	TTCAGGGTAT	CTCATT	60
AGGTGGGGGT	GGCAGGTGTA	TTTCTTTTT	AAACAATAAA	AGGCATTTAA	GTAAAAC	120
AATGAAAAAA	GTAGGCCCTC	TGACATTGTG	TACTGGTGG	TTCTGTCCCT	CTGCCTGTAA	180
CAAATCTCAT	TTTTGTTACC	AAGAACTGTA	TGAAAGAAGT	AAATCCACCC	CTCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 493 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(iii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

GAATTCCGCC	AAAGAGGCCT	ATGCCTGTGT	TGGGTTGACA	GTGAGGGTAA	TAATGACTTG	60
TTGGTTGATT	GTAGATATTG	GGCTGTTAAT	TGGTGTGTGTA	GAATATTGGA	GCACAGGTGG	120
AGTAGAAACA	AATCACAAAG	ACTTAACCGA	GTTGAGGTAT	AATGAAAGTC	TCACAAACTT	180
CAGCTGTCA	GGGAAGAAATG	GAACCAACCA	TGGAAGGATC	ACTCATGGTT	TCAAGTTACA	240
GAGTGCTAT	GAGAGTGGCC	TGATGCCTTA	CACGAATTAC	ACATTGATT	TCAAGGGTAT	300
AATAGACTAC	ATTTTCTATT	CTAAACCTCA	GCTGAACACC	TTAGGCATCC	TGGGCCCTCT	360
GGACCAACAC	TGGCTGGTTG	AGAATAACAT	CACTGGCTGC	CCGCACCCCC	TCATCCCCTC	420
TGACCACTTC	TCACTTTTG	CACAACGTGA	GCTCTTACTG	CCTTCCCTGC	CCCAAGTCAA	480
CGGCATTCTC	GAG					493

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

GAATTCCGCC	AAAGAGGCCT	AAGAAATCAA	AATTAAAGCA	ATCAAATAAT	ACTCACATT	60
ATATAAGAA	TACTTCAATT	TACTTCCAA	TGACTAAAGT	TTTATATTAA	ATGTTTAAT	120
ATTTCATATT	TTAGTTCTT	GCAATTATT	ACTTTCTCA	AAACCTACTT	AAATTAGCTT	180
TAAAAGTCTA	CTATATATAA	TTTGAAATT	TATTCAGTT	GCCTACAGGT	GTGTTTAAC	240
CACTGTGTAC	ATAGTATTAA	ACGGTCTGCT	TTTTTTTT	TAATATGGT	TCATGTNTGA	300
ACATCTGTAT	GTCATACTT	TTCTTGACAA	AGTTCTAAAG	GTTACTGTGT	TGAAGCATAAC	360
TGAAACGATTA	CTGATAATT	CTATTTGAG	GAACAGGTAT	GTCAGTTCTT	TCTCTCTGTT	420
TGATAATTCT	CTCTTTCCC	CTTAGGAATC	CAAAATCCT	TGTGGACTGT	CTTACTCCTG	480
ATTTCGAGG	TGATCTCAA	GCAATAGAAA	AAGTTGCTCT	GTCAGGATTA	GATGTGTATG	540
CACATAATGT	AGAAACAGTC	CCATTGCTCG	AG			572

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

GAATTCCGCC	TTCATGGCCT	ATCGAGATAC	GCTTTCGGCC	ACCAAGGTACG	CCTGGTGTMT	60
CTTTGTGGTT	TTTCGGATTC	TTTTGGGA	GTGCGGGAG	TCACAGTTAG	AAGGCGGCCG	120
GGTGGTGTG	GAGGAAAGTG	CTGAGGTCCA	GAGCGTAGTC	CGAGGGCTCC	GAAGTCAGAT	180
TAAAGGGCTC	GAG					193

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

GAATTCTGGCC	TTCATGGCCT	ACATAATGAT	GCTGCCTCAA	AACTCGTGGC	ATATTGATTT	60
TGGAAAGATGC	TGCTGTCATC	AGAACCTTTT	CTCTGCTGTG	GTAACCTTGC	TCCTGCTCCT	120
GAATTCCCTGC	TTTCTCATCA	GCAGTTTAA	TGGAACAGAT	TTGGAGTTGA	GGCTGGTCAA	180
TGGAGACGGT	CCCTGCTCTG	GGACAGTGG	GGTGAAATT	CAGGGACAGT	GGGGGACTGT	240
GTGTGATGAT	GGGTGGAACA	CTACTGCCTC	AACTGTGTG	TGCAAACAGC	TTGGATGTCC	300
ATTTTCTTT	CGCCATGTTT	CGTTTGGAC	AAGCCGTGAC	TAGACATGGA	AAAATTTGGC	360
TTGATGATGT	TTCCTGTTAT	GGAAATGAGT	CAGCTCTCTG	GGAATGTCAA	CACCGGGAAAT	420
GGGGAAGCCA	TAACTGTTAT	CATGGAGAA	ATGTTGGTGT	GAACTGTTAT	GGTGAAGCCA	480
ATCTGGGTTT	GAGGCTAGTG	GATGAAACA	ACTCCTGTT	AGGGAGAGT	GAGGTGAAAT	540
TCCAAGAAAG	GTGGGGACT	ATATGTGATG	ATGGGTGAA	CTTGAATACT	GCTGCCGTTA	600
TACTCGAG						608

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 518 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

GAATTCTGGCC	TTCATCGCCT	ACAGCGCTGC	CTTTCCTTAT	GAAGAAGACA	CAAACTTGGA	60
TTCTCACTTG	CATTTATCTT	CAGCTGCTCC	TATTTAATCC	TTTCGTCAA	ACTGAAGGGA	120
TCTGAGGAA	TCGTGTACT	AATAATGAA	AAGACGTAC	TAATTTGGTG	GCCTAATCTC	180
CAAAAGACTA	CATGATAACC	CTCAAATATG	TCCCCGGAT	GGATGTTTIG	CCAAGTCATT	240
GTTGGATAAG	CGAGATGGTA	GTACAATTGT	CAGACAGCTT	GACTGATCTT	CTGGACAAGT	300
TTTCAAATAT	TTCTGAAGGC	TTGAGTAATT	ATTCCATCAT	AGACAAACTT	GTGAATATAG	360
TGGATGACCT	TGTGGAGTGC	GTGAAAGAAA	ACTCATCTAA	GGATCTAAA	AAATCATTCA	420
AGAGCCCAGA	ACCCAGGCTC	TTTACTCCTG	AAGAATTCTT	TAGAATTTT	AATAGATCCA	480
TTGATGCCTT	CAAGGACTTT	GTAGTGGCAA	ATCTCGAG			518

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

GAATTCTGGCC	TTCATGGCCT	ACCTTGATAC	ATCAGCTGAC	CTCAATTCCG	GATACCTTT	60
CCCCCCCCGAA	AACTACAACA	TCTGGCCCG	CCCAGCCGA	AGACAGATCG	TCGCTCCCTG	120
GACAATCAGA	CGAATTCTCC	CCCCCCCCCG	AAAAAAAAG	CCATCCCCCC	GCTCTGCC	180
GTCGCACATT	CGGCCCCCGC	GACTCGCCA	GAGCGCGCT	GGCAGAGGAG	TGTCCGGCAG	240
GAGGGCCAAC	GCCCGCTGTT	CGGTTTGCAG	CACCGCAGCAG	GGAGGTGGGC	GGCAGCGTCG	300
CGGGCTTCCA	GACACCAATG	GGAATCCAA	TGGGAAAGTC	GATGCTGGTG	CTTCTCACCT	360
TCTTGGCCTT	CGCCTCGTGC	TGCATTGCTG	CTTACCGCCC	CAGTGAGACC	CTGTGTCTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

GAATTGGCC	TTCATGGCCT	AAGAGATTAA	GTGATTTACT	CAAGGTCATA	TTCCCTGGAA	60
GTAGCAAAAC	TTCTGGACCA	GATTCTGTAT	TCCAAAGCG	GTACTGCTTG	TACAACACTC	120
TGAGAAGTAA	TTACTGTGGA	GCAAAGCAA	AAGAAGTCA	AAAGCAGGTG	ATAGGTGTAG	180
ATTTACATAG	TGTAAGGGTA	GGCTAAAGTG	TTGTAACAAA	TGCACCCCTCA	AGTAGGTAAT	240
GGCTCAACAA	CAATAGATGT	TCACTTCCC	CATCTCAGAG	CAAATGGGT	TCTCCTCATC	300
AGCTAAAGCT	TTCCTACATG	GGATGATTG	GGGAGCAAGA	CACTCCATCT	ATGGCTCCCT	360
TACCCCTCAA	GGCCCTCTTA	TGTCTTAT	GTAACCAGTG	GAAGAGCTCG	AG	412

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 574 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

GAATTGGCCT	TCATGGCCTA	GGCTTCTTCG	GAGCTGTGTA	NTCTTAATT	GCTTTGCTGC	60
TGGCTGGCTG	ACAGCTGATG	GGGGACTCCT	CANGACGGAC	TCCCTCCAG	ATGCACCCAT	120
CTCCATCCTT	CTCAACTCCC	CAACCTTGT	CCTCCCCACT	CTTCGCTCGC	GGGGCGGTCT	180
GAGACCACCA	GGACCAGTTT	CAGGGTTTC	CTTCTCCAGC	GAGACTTGGC	AGAACAGGCT	240
TTAAAAGCAA	AGGAGGCAGC	CGAACAGTGT	GAATCCCTT	GGACAATTGA	TGATATTAT	300
CATTGTGCC	AGTTCTACA	AATAAAAGAT	GGGTGGATTA	TTTTCTCGAT	GGAGGACAAA	360
ACCTTCAACT	GTAGAAGTTC	TAGAAAGTAT	AGATAAGGAA	ATTCAAGCAT	TGGAAGAATT	420
TAGGGAAAAA	AATCAGAGAT	TACAAAATT	ATGGTTGGA	AGATTAATTC	TGTATTCTC	480
AGTTCTCTAT	CTGTTAACAT	GCTTAATTGT	ATATTGTGG	TATCTCCTG	ATGAATTAC	540
AGCAAGACTT	GCCATGACAC	TCCCCACATCT	CGAG			574

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

GAATTGGCC	TTCATGGCCT	AGGCGCGGCC	CGGGTTCCCG	TTCCCCGCGG	AGCCATGCGG	60
TACAACGAGA	AGGAGCTGCA	GGCTCTGTCC	CGGCAGCGG	CCGAGATGGC	GGCCGAGCTG	120
GGCATGAGGG	GCCCCAAGAA	GGGCAGCGTG	CTGAAGCGGC	GGCTGGTGAA	GCTGGTGGTG	180
AATTCCTCT	TCTACTTTCG	GACAGACGAG	GGCGAGCCCT	GCTGCTGGAG		240

CGCTGCAGAG TCGTCCGGGA AGAGCCCGGC ACCTTCTCCA TCAGCTTCAT TGAGGACCC	300
GAGAGGAAGT ATCACTTCGA GTTCAGCTCG AG	332

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

GAATTCCGCC TTCATGGCCT AATTGCAAGA TCACGGAATC TCCTGAATCA TTAAGAAAAG	60
ATAAAATATC ACAAGCATCT TTAGTGTATT GTGTATTTCAG TAATTCCTTG GAGTTGTATT	120
TATTAAGCTT ACCAGATTTT AAAGGCATAT AAAATGTGGT AAGATATGAG ACACATACTG	180
AAATATCAGT GCAAAGGGAG AATGGTAGTT GAATGGTCAG AAACGAAAAA GCCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

GAATTCCGCC TTCATGGCCT AGAACATTT TTGTTATTG TGAAACATTT TTATACCTTC	60
ATTATAATTG GTTGAGCCTA GAGTTGGCT ATTTGAATAT TTATTATGAT AATCTTTG	120
CTAATGGTAA CAGCATATCT TGTCTAACAA AAATTACTGT TAACAGCAAT CGAACTCGAG	180

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAATTCCGCC TTCATGGCCT ACTGAGATCC AGACCAGCTC CTCCCAGACC TCTCCAGAAAG	60
AAGCCATGGG AACCCTCGT ATCCAGCATT TGCTGATCCT CCTGGTCCTA GGAGCCTCCC	120
TCCTGACCTC GGGCCTAGAG CTGTTTGTC AAAAGGGTCT GTCCATGACT GTGGAAGCAG	180
ATCCAGCCAA TATGTTAAC TGGACCACAG AGGAAGTGGA GACTTGTGAC AAAGGGGCAC	240
TTTGCCAGGA ACCATACTA ATAATTAAAG CAGGGACTGA GACAGCCATT TTGCCACGA	300
AGGGCTGCT ACCGGAAAGGG GAGGAGGCCA TAACAATTGT CCACCACTCT TCACCTCCCG	360
GCCTGATCGT GACCTCCTAC AGTAACTACT GTGAGGATTG CTTCTGTAAT GACAAAGACA	420
GCCTGTCTCA GTTTGGGAG TTCAGTGAGA CCACAGCTTC CACTGTGTCA ACAACCCCTCC	480
ATTGTCCAAC CTGTGTGGCT TTGGGGACCT GTTTCACTGC CCCTCTCTT CCCTGTCCCCA	540
ATGGTACAAC TCGATGCTAT CAAGGAAAC CTCTCGAG	578

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

GAATTGGCC	TTCATGGCCT	ACATGAATCC	ACTCCTGATC	CTTACCTTTC	TGGCAGCTGC	60
TCTTGCTGCC	CCCTTTGATG	ATGATGACAA	GATCGTTGGG	GGCTACAAC	GTGAGGAGAA	120
TTCTGTCCCC	TACCAAGGTGT	CCCTGAATT	TGGCTACCAAC	TTCTGTGGTG	GCTCCCTCAT	180
CAACGAACAG	TGGGGGTAT	CAGCAGGCCA	CTGCTACAAG	TCCCGCATCC	AGGTGAGACT	240
GGGAGAGCAC	AAACATCGAAG	TCCTGGAGGG	GAATGACAG	TTCATCAATG	CAGCCAAGAT	300
CATCCGCCAC	CCCCAATCG	ACAGGAGACT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

GAATTGGCC	TTCATGGCCT	AGGGCACAC	TGAGTTCACT	ACTTCAAAAT	TGCCGTGCTC	60
TACCTCTCCC	CACTGCACAA	AAACACTCTC	CACACCAAC	TGCTGCTGCT	GGGGGATGGG	120
GGGATGGCGT	CAGCGATTCA	AGACTGTTT	TCCTACCTGT	TCAGCACCTTC	TTTCAGCGAT	180
ATGAAGTTAA	ATCCAGTCTT	TCCCTGTCTC	CAGGCATCAT	CGCCATCAAC	ATACAGCCAT	240
ACTCCAGGAT	TGCCCCATTT	CAACATAAAC	GGACTCTCTT	GGACTCCACT	TCCACATCA	300
GTCACAGCCA	CACTTCCTGA	GAAAGAAGTC	TACACTTTTC	ATTCACTTTC	ATTCAACCCAC	360
TGCTCGAG						368

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

GAATTGGCC	TTCATGGCCT	AGAGAAAATA	AAGAGTTATA	TCAGAAATT	ACAAACATAA	60
CTTTTTAAAT	TTTAAATTGC	AAAATATATA	TCATACGAA	ATGAAAATT	TAATTCTTCT	120
TGGATTCCCTG	GGAGCCACAT	TGTCA	CTTATCCCA	CAGCGTCTCA	TGTCTGCCAG	180
CAATAGCAAT	GAGTTACTTC	TTAATCTTAA	TAATGGTCAA	CTTTGCCAC	TACAACCTCA	240
GGGCCCACTT	AATTCACTGGA	TTCCACCTTT	CTCTGGAATT	TTACAACAGC	AGCAGCAGGC	300
TCAAATTCCA	GGACTCTCCC	AGTTCTCTTT	ATCAGCTCTA	GACCACTTTC	CTGGACTGCT	360
CCCAAAATCG	ATACCCCTAA	CAGGAGAGGC	CAGTTTGCC	CAAGGAGCCC	AGGCAGGCCA	420
AGTTGATCCC	TTACAGCTTC	AAACACCGCC	TCAGACACAA	CCAGGCCAC	GTCTCGAG	478

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GAATTCTGGCC	TTCATGGCCT	ACTTACAGAA	CCTATTCACT	GGGAAGGAAG	CCCTCATTAT	60
AATGATTTTC	ATTCTTATGT	GTGTTTCAGG	ACGACTGGGT	TTGGATTAG	AAGAGGATTA	120
TTATACACCA	CAAAGGTGG	ATGTTCCCAA	GGCCTTGATT	ATTGTTGCAG	TTCAATGTGG	180
CTGTGATGGG	ACATTTCTGT	TGACCGTGC	AGGCAAAGTG	CTGGCCTGTG	GACTCAATGA	240
ATTCAATAAG	CTGGGTCTGA	ATCAGTGCAT	GTCGGAATT	ATCAACCATG	AAGCATACCA	300
TGAAGTCCC	TACACAAACGT	CTTTTACCTT	GGCCAAACAG	TTGTCCTTTT	ATAAGATCCG	360
TACCATTTGCC	CCAGGCAAGA	CTCACACAGC	TGCTATTGAT	GAGCGAGGCC	GGCTGCTGAC	420
CTTTGGCTGC	AACAAGTGTG	GGCAGCTGGG	CGTTGGGAAC	TACAAGAACG	GTCTGGGAAT	480
CAACCTCGAG						490

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GAATTCTGGCC	TTCATGGCCT	AGAAAAAAGA	AACTGTCGTG	GATACTGTCA	GTGTATATAT	60
TTATGTTGTA	CCTGAGAGCC	ACCCCCAATT	AGATTGACTT	TAGATCGTTT	ATACAAAAAT	120
AGCTTGAAGA	ACTGTTTTTT	CCATGGTAA	TGCTTTTGAA	TATTAACCTA	GTATGTTAG	180
ATTCCTACCT	CAGTGGTACT	GTCACAGCCA	TTGGTTACAT	TTCTGAAACC	CTTCAGAGTA	240
AGAGTTTGG	TTTTTTGTTT	TGTTTTGTTT	TGTTTTTGAA	GATGGAGTCT	TGCTCTGTGCG	300
CCCAGGCTGG	AGTCACTGCA	AGCAACCCAG	GTGGAGTCA	GTGCAACCTC	CCCTCCCAG	360
GTTTAAGCGA	TCCTCCCTAAC	CTCGAG				386

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

GAATTCTGGCC	TTCATGGCCT	AGCTTCAGTA	GCAAATAAGG	ACATCATCTG	CTATAACCTA	60
CAAGCAGTTG	GACAGATATT	CTACATTCTC	TCATTCTCT	ACACCGTCAA	TTACATCTGG	120
TATTTGTACA	CAGAGCTGAG	GATGAAACAC	ACCCAGAGTG	GACAGAGCAC	ATCTCCACTG	180
GTGATAGATT	ATACTTGTGCG	AGTTGGTCAA	ATGGCCTTTG	TTTCTCAAG	CCTGATACCT	240
CTGCTATTGA	TGACACCTGT	ATTCTGTCTG	GGAAATACTA	GTGAATGTTT	CCAAAACCTTC	300

AGTCAGAGCC ACAAGTGTAT CTTGATGCAC TCACCACCAT CAGCCATGGC TGAACCTCCA	360
CCTTCTGCCA ACACATCTGT CTGTAGCACA CTCGAG	396

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GAATTCGGCC TTCATGGCCT ACACCTTTCA CTTATCTTAT AGTCACTTAA TTCCTCTACT	60
CTTATCATTT GATATTTCA TTTTATTGTG TATCTCTGTN NGGCCAAATC AATAGATTTT	120
GAACAACTCTC ACACCTAACCC TTTTAAAAAA ATCTAATAGG CCCAGTTTCC TCTCAACAAAT	180
CTTGTAGAGAA CCTTCGAGAA AGGAGAAACA CAGACCTCCC GCTTCTAGAC ATGCACACTG	240
TAACCCGGGA AGAGGGAGAA GGCGATGGAGA CAACTGATAC GGAGTCTGTG TCTTCCGCCA	300
GCACATACAC ACAGTCTTTA GAGCAGCTGC TAACTCTCC CGAAACTAAA CTTGGTATGT	360
TACTCTGTCT AAATATGTTT TTCTTATTTA ATTTCACTGT CTTATTTAAT TACTANTACT	420
CTAAGTTACA TATGTTTTT NGGGCTGCTC CAATAAAATT TCTTCAATA TTCCACTACC	480
TGTTGTATT AGGTTCTCTA GAGGGACACT CGAG	514

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

GAATTCGGCT TCATGGCCTA GGTTTTCTGT ACATGGAGAT TAAACTGTCT TCCAAAGTGA	60
AGAGTTTATT GTTCTAGATC TTGAGCACAA AGGTTGGTAT ACGTTAATAA AAAAAATAGC	120
AAGGGAAGAA AATCATTTC TTCATACCAA GTAAGAGAGC ACTTATCATG GTAGGCACTG	180
GCTTGTCAAT TATGAGACCA GTAGTAGAAA TAGCTTGTCT TTCTCAATT TTCTGGAGT	240
ATTCTTCAGA CTTCTTTAC ACTGCTCAAG GTGGGGCGAG TGGCAGGGCG GACCCTGGCG	300
ACCTGACGCT GCGGAGGCTC GAG	323

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

GAATTCGGCC TTCATGGCCT AGGAACAGTG TGTTTTTG TGTTGGCTT GCATTCTCTC	60
CTCCGTTTTT GGAGCAGCGT GAGATTATG CAATGCTACA TTTCCTCCCT CTGCGCCCTC	120
CTACCCCCATC AATGTCTCAT GGGTGGTGTG ATAGAGGCTA TGGGAGTGAA GACCACTGGT	180

GTTAGTCTGT GTATAGTTCC TGGGGTGTGG CGAGTACCAAG CTCTGACAGC GGAAGAGAAC	240
TATACTGTTG ATCCCATTA TTCTCAGTAG GTGTGTTCTA TAAAATTGCT CGGAACACCA	300
AATTAGCGAA TCCTGAACCA TCGTTCCAG AGGAATAGGG GGTTAGGGTC CTGTGATCCT	360
CAAGTGCAA CATTGTCTTC GACTGATTAA TATGTAACCT TGTTTATAT GTGCAATCTC	420
GAG	423

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

GAATTCGGCC TTCATGGCCT ACCGAAACCA AATAATTCAA GCACTGCTTA TTACAATTTT	60
ACTGGTCTC TATTTTACCC TCCTACAAAGC CTCAGAGTAC TTGAGTCTC CCTTCACCCCT	120
CGAG	124

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

GAATTCGGCC TTCATGGCCT ACATCTATGA CTTTTTAAAC ATGGGGCGTT TTGTGAATAT	60
CATGATAATA ACAAGAGTCA ACAGGCTAAG TGAGAGGAGA GGGATGCTAC GCCTACGCTG	120
CCCCCAACAC GGCAGCCGG CTTCTGCGCC TTTGGTGTG GATTTCTTT GTGATTTAC	180
GGGGTTTTGT GTTTTTTTT TCTTGTTTT TGTTTGTAA TTTTTCTTG TCCACTTGAT	240
TTGCATGCAA CACCCACAAA AAGGAAACAC AAAACCCCGT CTGCTCGAG	289

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

GAATTCGGCC TTCATGGCCT ACACATGAG AGGACCGATT GTATTGCACA TTTGTCTGGC	60
TTTCCTGAGC CTTCTGCTTT TTCAGCGTTG CCACACAATG TCTGGCCTTC CCCAAATAG	120
AAAGGAGGAG GGAGATAGCA CATGTTCATG CGGAAAAGG GCAGTCCGAT AAGATGAACA	180
CCGATGACCT AGAAAATAGC TCTGTTACCT CAAAGCAGAC TCCCCAACTG GTGGTCTCTG	240
AAGATCCAAT GATGATGTCA GCAGTACCAT CGGCAACATC ATTAATAAA GCAAAACTCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

GAATTCGGCC AAAGAGGCCT ATTTTTTTT CTGCAAACAC TGTGTATAGT GAGACTTGTT	60
CTACTTGGAA GAACAGGTAA CCTTTGAAA ATGAGGTGA GTTCTTCCT TTCTGATGCA	120
TTCATTTTG AAGATTTTTT TTTCCTCCCT CCCCTCTCCC TCGAG	165

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GAATTCGGCC AAAGAGGCCT AGCTTCTTTG TATAATTAAA TCTGAGTTT GTTGAGCAT	60
CTTCAACAT GTACCATATT TATGACAACT CTCTTCATA GGATCTATCT GTCTGCAAC	120
AAGTATTGAT CTTACAGTAA AATTTTCAC AAATTCATTA GATTCTATGT CTCTTTTCT	180
GGTAGGAATT TTGTGCGAGG TAGCTATCTC TTGCCCTAGA TTATTCTCCT TGTTAGCTG	240
CTGATTCTTA AACTGGCCTC TAGATTCCA GATTCTTCC GGTACAGACT TTCTCTTGC	300
AAGTTCTTCC ATCTCTAATC TTGAGATTA ATCTCTTTT GAAATGCTCCT GCTGCTCTAC	360
TCTTGATGTT CTCGAG	376

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

TCTCCAAGGG AAAATAATG CTTTTACTAT CTAGTTGTC TCTTTGAGAA TTAAAACCTCT	60
TTTTTTTTT TTTCATTCCA GTAGCTTTG GGGTAGAGTT TGGCTTTG AGAATTGCA	120
ACTAATTAAT TTAGGGGTG ATTTGTACAT CATCTCTATA TTCTGAAAC ACAGTAGAAA	180
CAGCCAGCAG TCAGGCAACC ATCTACCATG ACCATTTAA CATCCCCAAA GTGAAACACC	240
AGATGTGATC TGCTAGATT AGTGGAGGCG GCTGGCTCGA G	281

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

GAATTCCGCC	AAAGAGGCCT	AGCTAGNCTT	GCTCAGCTTT	GTGGATACGC	GGACTTTGTT	60
GCTGCTTGCA	GTAAACCTTAT	GCCTAGCAAC	ATGCCAATCT	TTACAAGAGG	AAACTGTAAG	120
AAAGGGCCCA	NCCGGAGATA	GAGGACCACG	TGGAGAAAGG	GGTCCACCAAG	GCCCCCCAGG	180
CAGAGATGGT	GAAGATGGTC	CCACAGGCN	TCCTGGTCCA	NTGGGTCNTC	NTGGCCCCCN	240
TGGTCTCGGT	GGGAACCTTTC	CTGCTCAGTA	TGACGGAAAA	GGAGTTGGAC	TTGGCCCTGG	300
ACCAATGGGC	TTAATGGGAC	CTAGAGGCC	ACCTGGTCA	GCTGGAGCCC	CAGGCCCTCA	360
AGGTTTCAA	GGACCTGCTG	GTGAGCCTGG	TGAACCTGGT	CAAACCTGGTC	CTGCAGGTGC	420
TCGTGGTCA	GCTGGCCCTC	CTGGCAAGGC	TGGTGAAGAT	GGTCACCCCTG	GAAAACCCGG	480
ACGACCTGGT	GAGAGAGGAG	TTGTTGGACC	ACAGGGTGCT	CTGGTTTCC	CTGGAACCTCC	540
TGGACTCCT	GGCTTCAAAG	GCAACCTCGA	G			571

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

GAATTCCGCC	AAAGAGGCCT	ATGCGCAAGG	ATCAAGCCGA	CTACCTGTGC	TGTCTACTGG	60
GACAGCAGTC	TCCGAGCTAC	TCGGTACCTC	CCTCTGCCAG	GTGCGTGGAGT	TAGGCCCCAG	120
TCCCTACTTG	TCACTGGTTC	CCACTGTGCT	CCTAACTGTG	CAGCACCTGG	GAGCTCTGGC	180
CTGGGGCTGG	AGGCCCTGGT	AGGAGCTGCA	GTTGGAGGCC	GTTCCTGTGCC	CAGCAGGGT	240
GAGCGGCTCC	CATGGGCCCT	GTGCTGCGAG	GGAGGCCAGGG	CTGGGGCACA	TGTGCTGTGA	300
AACTGGCACC	CACCTGGCGT	GCTGCTGCCG	CCACTTGCTT	CCTGCAGCAC	CTCCCTACCCCT	360
GCTCCGTGTC	CTCCCTCTCC	CCGGCCCTGG	CTCAGGAGTG	CTGGAAAAGC	TCACGCCCTCG	420
GCCTGGGAGC	CTGGCCTCTT	GATATACCTC	GAG			453

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

GAATTCCGCC	AAAGAGGCCT	ATGTCATGAG	TGAACTTGGC	AATTGCCTTG	TTAAAACCAAG	60
TTGGACATTA	TCTTCCACAT	TGCGAAGCTA	TACATGTCTG	ATATGTTCTG	AAAGAATAGA	120
ATTTATAGTT	AGATATACTA	TTTTGATTA	TTTACTCAGA	AGGAGACATG	TAATTATTCT	180
TATGTTGTCA	TGAAAATCTA	TTAAATGCAT	TTATATTCTA	CATCAATGTT	ACGAAGTCC	240
ATTATTATTA	TTTTACAGAG	GGGAAGCCAA	GATACAGGAG	TGAAATTAC	TTGGCCTATC	300
GCTCGAG						307

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

GAATTCTGGCC	AAAGAGGCCT	AAGAAGATGA	ACAAGGCCA	GCTCTATTAC	CAGGTTTAA	60
ACTTTGCCA	TGATCGTGT	TTCTGCAC	ATGATATGGA	AAGGCTTGAT	CGTGCTCACA	120
GGCAGTGAGA	GCCCCATCGT	GGTGGTGTG	AGTGGCAGTA	TGGAGCCGGC	CTTTCACAGA	180
GGAGACCTCC	TGTTCTCAC	AAATTTCCCG	GAAGACCAA	TCAGAGCTGG	TGAAATAGTT	240
GTTTTAAAG	TTGAAGGACG	AGACATTCCA	ATAGTTACA	GAGTAATCAA	AGTTCATGAA	300
AAAGATAATG	GAGACATCAA	ATTTCTGACT	AAAGGAGATA	ATAATGAAGT	TGCTCTCGAG	360

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

GAATTCTGGCC	AAAGGGGCCT	ACCTGAAACG	GCAGTCCGGT	CCCTCCGACA	TITGCCAGCG	60
GAAGGCCCTGG	GCTTCACACT	CTGTGCCCTCC	CGCGCCTACC	TGGCACGATG	CCGAGCACAC	120
AGCAGATGCT	CAATGAATGC	CCAACCAACC	CTATACTCTGG	CTTGGATCTC	AAGCTCCCTG	180
GCCGGGGCCT	GATGGAAGGC	TTTGGGGCA	CAGGAGGCTG	CCCCCTTGGG	CGCCCCCGGC	240
CACCTCTTCG	CCCTCGAACATC	TCAGGCAGCT	TGGTCAGGAA	CTTCTCTCC	ACGTATTTAG	300
CGTGAATCCA	GGCCTCCCTTC	TCCTGCCCTGT	GGGAGGGGAG	AAGCACGCAG	TCTTCCCTCT	360
TCTGCTCCAG	GGGTCCCCCA	TTCCCTGGG	AGGCTAAACC	CATAGCTCGA	G	411

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

GAATTCTGGCC	AAAGAGGCCT	AGGGAGTGT	TGCGTTCTT	CTCCGTTGG	CAGTGAAACA	60
CATCTCAGAA	AGGTGGAGCT	GATCAGAAATA	ATGTTAGCA	TCAACCCCT	GGAGAACCTG	120
AAGGTGTACA	TCAGCAGTCG	GCCTCCCTG	GTGGCTCTCA	TGATCAGCGT	AAGGCCATG	180
GCCATAGCTT	TCCTGACCCCT	GGGCTACTTC	TTCAAAATCA	AGGAGATTAA	ATCCCCAGAA	240
ATGGCAGAGG	ATTGGAATAC	TTTCTGCTA	CGGTTCAATG	ATTTGGACTT	GTGTGTATCA	300
GAGAATGAAA	CCCTCAAGCT	CGAG				324

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

GAATTGGGCC	AAAGAGGCCT	AGTGGGGCTG	TATTTAATA	CAAGAAAGAC	ATTGCTCTAG	60
AACATGGCTC	GCCTTTCGTT	CAGGGCTAG	CAGTTTATT	TAGCCATAAG	GGTAAGGGAG	120
CAGGTCAAGAA	ATGACTTTTA	GTGTAATCT	ATCTGTAATT	AAAAATACAA	ATGCTGTCAT	180
AAGATCAAAT	GTATCAAAA	ATCAGTATT	AAAATTAAT	TTACCCCCAA	ATTCCTTCA	240
AAAAAGTTGT	AATGTTCTT	TTCACTGAAG	CCTTGCCT	GCTAGAGCTG	AAGAATGTGA	300
TCAATCGGCT	TGTGAATAA	TCCCGCACAG	TTGGTATTCC	GCTGAAGCCA	ACTCTAGCTG	360
GGGGCTCGAG						370

(2) INFORMATION FOR SEQ ID NO:262:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

GAATTGGGCC	AAAGAGGCCT	AAGAAATAGG	ACTATACAAA	TTTTCAACTT	CTTTTGATAT	60
CAGTTTGGT	AAGATGCATT	TTTCTTCGTA	GAATTGTTT	CATTGAAATT	TCCAAATTTA	120
TTAGCATGAA	GTGTTAATA	AAAATCTTAT	ATTTTACTC	AAATTTGAG	ATAGTTGTAG	180
ATTTACATGA	AGTTGTAAG	AATAATAGAA	AGATCCTGTG	TACCTTTCC	CAGTTTCCC	240
CAAAAGTAAC	ATTTGCTATA	ACTCTAGTAC	AGTAGCACAA	CTCGAG		286

(2) INFORMATION FOR SEQ ID NO:263:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

GAATTGGGCC	AAAGAGGCCT	AGGCAAACCG	TGTACTAAGC	ATCAGTGCAG	AGATAGTGAA	60
TGAGACACAG	TATTCCCACC	TTTGAGCAGT	GCCAGTCTAG	TATTAGAATA	TTTTGGCTA	120
AAAAATTATT	TTGAAGCATA	AAGAAGCTTT	TGTTTGTCT	GGTGATTTTC	ATAACATATT	180
CACATTCTTA	ATGTATTTTT	GGTTTTTCAG	AAAGTTACTT	CTGGCCTGTG	TTCTTTCAGA	240
ATATAGGTG	CAGCTTGTGT	TAAGTGCAGG	AACTATTGAT	AGACTGAGTT	TAGAAGAAGG	300
GAAACTCGAG						310

(2) INFORMATION FOR SEQ ID NO:264:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

GAATTCTGGCC	AAAGAGGCCT	AGGACTTTGG	GGCAGGGTGT	TAATTTATA	TAGGTACCTC	60
AAGAAAAAGA	ACCTGAATAT	GCTGCATTTT	CTTCTTTAG	CTTTACATG	TAGCATTG	120
TTTGCTTTT	GTATTTTG	TTTGATATA	TGCTTTGG	ACCCAATAG	ACTGTTGAAA	180
GAAATTTAAA	AAATTACTCTT	GTAGGGATAT	AGTATCCTA	AAAAATAAAA	ATTAAAAAAA	240
ATTTAAAAAA	ATTGCTGAA	TATCTGGCTC	GAAGGTTGCC	CTATATTAGA	ATAATACCTT	300
AGCCAAACAC	ATCAGCTCGA	G				321

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 550 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

GAATTCTGGCC	TTCATGGCCT	TGTGATTCTG	CAAAGGAGGA	ACAATAATT	ACTGTTTCCC	60
AAACTTATCT	GACCATAGAA	CATATNTCTC	AGAGTATTTT	TCAAGAGTAG	TATTTTCTGT	120
AATATATGAT	AAAAATAAT	CGTATCGGCC	ATCTTTGTAC	ATAAGGTCAA	AATGTCAGCC	180
AGCCCTGAAA	AAATGCAAG	CCAAAAGGTA	GAGAGATAAG	TGAATAAAGC	TGGCACACTG	240
TCAGTCGGGA	GTACCATGCT	GCATTCTGAG	TCAAGCTCCA	GGAAACTGAG	CTAGGGTTTG	300
TCTCTAAGAA	AAAAACTGG	AGCGTCCAAA	GCTTCTGGAT	TCCATTTAAT	AAAACCCCTT	360
TTAAATTAAA	TCCCTGTAAAC	TGAAGAGTAT	CGGTGGATGA	AGAAAAAATA	GTCTCACATG	420
TCTTCATTT	CATCCTTGGC	TCAGTACAGC	TCCAGTTCCA	TTATTCTTAA	ACATCTATTA	480
ACATGATTGC	AAATAATTA	CACAGGCTAA	CTGCCAAGCA	TTTTTACAG	GAAGCAAGGC	540
ACTGCTCGAG	G					550

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GAATTCTGGCC	TTCATGGCCT	AGTTAAGTGG	GAAGTTAAAT	GGCAAGTACT	AGAATGCCAC	60
CTATGGCAAG	CACTAGAATG	GTCTAGGTGT	GAATGAGGG	AGTAATGTCA	GGGAGTCAAG	120
GTGCCATCC	ATAGCAGTGA	TTCTTATCTG	GGGTAGGGGG	TGAATTTCAC	GTGGAGGGAG	180
GTCTCTGGAC	ATGGACCCCC	ACGCAGGGCT	ATCCAATCAT	CTGAGGGGTG	AGCAGTGTTC	240
AGCTCAGTAA	AAAGTAAGGGA	AAAAAAATAG	CAGTCTCTAA	AAGGAACATA	GAGCGCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

GGGGAGAGCA TCAGGAAGAA CAGCTAATGG ATGCTGGCT TAATACCTAG GTGATGGAT	60
GGTCTGTGCG GCAACACCCA TGGCACAAAGT TTACCTATGT AACCTGCACA TCCTGACATG	120
TACCCCTGAA CTTAAAATGA AAGTTGGAGA CCAAAAAACA AAACACCATA AAACTACAAA	180
ACTTCCTAAA CAATAAACTA GTAGAAAATT TCTAAAATAT ATAATTCAAG AATTATATAA	240
GAGCTTTT TATATGTAAA TATAAATTAA AATACAAGAG AAACATCTAA AACAGGTTGC	300
TTCTGAGAAA CGTGACTGGT TATTAAGAAG AGGTATATAG GGGCTCACTC GAG	353

(2) INFORMATION FOR SEQ ID NO:268:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

CATTATTTAA CCTTTTAAAC AATCAAGAGA TTGCTTTTA AATTGTCTCT AAAAGGTTT	60
GATTTTTTAC GAAAGAGAGA GCACTTGAAT ATATCTTAT GTACCACCGT GTCTTTTTT	120
GTTAGATTT TCATCTGTGG GTATAATATA AAATATTCTT AAAATGAAAG CTTTACGCTT	180
GTGTTTGAGA CTAAGCAACT TGCATTGTGT CATGACCCCTT CTAATACACAA AACCCCTCGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:269:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GAATTGGGCT TCATGGCCTA CACTCAACCA CTGAAAAGC TGAAAATCAA TGTAAAAAAG	60
GTTCACAAAGT GTGCCGTGTG TGGCTTCACC ACCGAAAACC TGCTGCAATT CCACGAAACAC	120
ATCCCTCAGC ACAAAATCGGA TGGTTCTTCC TACCACTGCC GGGAGTGTGG CCTCTGCTAC	180
ACGTCTCAGC TCTCTCTGTC CAGGCACCTC TTCATCGTAC ACAAGTTAAA GGAACCTCAG	240
CCAGTGTCCA AGCAAAATGG GGCTGGGAA GATAACCAAC AGGAGAACAA ACCCAGCCAC	300
GAGGATGAAT CCCCTGATGG CCCCTCGAG	330

(2) INFORMATION FOR SEQ ID NO:270:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

GGGGCACCA TTCCAGTAT GTACCAAACC AAAGCGTCA TCATTCGAAT GATCATCACT	60
GCGGTGGTAT CCATTCAGT CACCATCTTC TGCTTCAGA CCAAGGTGGA CTTCACCTCG	120
TGCACAGGCC TCTTCTGTGT CCTGGAAATT GTGCTCTGG TGACTGGGAT TGTCACTAGC	180
ATTGTGCTCT ACTTCCAATA CGTTTACTGG CTCCACATGC TCTATGCTGC TCTGGGGCC	240
ATTTGTTCA CCCTGTTCTT GGCTTACGAC ACACAGCTGG TCCCCGGGAA CCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

GCCAGACTAC CACAAGCCCC ACCCACACTA TGCCAAGCCC TACCCATACC ACAGCAAGCC	60
CCACTCATAAC TTCCACAAGC CCCACCCATA CCCCCACAAG TCCCACCCAC AAAACCAGTA	120
TGTCACCTCC CACCACTACA AGTCCCTACCC CCAGTGGTAT GGGCCTAGTC CAGACTGCCA	180
CAAGTCCAC CCATCCTACC ACAAGCCCCA CCCATCCCAC CACAAGCCCC ATCGTTATAA	240
ATGTAAGCCC TTCCACTTCT CTAGAACTTG CTACCCCTCTC CAGCCCCCTCC AAACACTCAG	300
ACCCACCCCT CCCAGGAAT GACTCCCTTC CCTGTAGTCC CCCAGTCTCC GATTCTACAA	360
CTCAGGCAGA CCCTATGGCC CCCAGAACTC CCCACCCAG TCTCGAG	407

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

ACTGAGCTCA AGGACCCCTC CAAGAAGAAG ATGCAGCACA TCTCCAACCT GTCCATCGCT	60
GTCATGTACA TCATGTACTT CCTGGCTGCC CTCTTGGCT ACCTCACCTT CTACAACGGG	120
GTGGAGTCGG AGCTGCTGCA CACCTACAGC AAGGTGGACC CGTTTGACGT CCTGATCCCG	180
TGTGTGGCG TGGCGGTGCT GACAGCAGTC ACGCTCACAG TGCCCATCGT TCTGTTCCCG	240
GTGCCCGCG CCATCCAGCA GATGCTGTTT CCAAACCAGG ACCTCGAG	288

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

GAATTCCGCC	TTCATGGCCT	AGTCAAGCTA	GGTAAGCTAA	AAAGAAGAAA	ACCTGGTTAC	60
AGCCCGGTGA	ATTGATTTTT	TTCCAGCCG	GAAATAGATA	TTTCTCTCAC	ATATAATTGG	120
AAAACTTTAG	TCATCTTCAT	AAAACCTTAA	AAGTTACCTA	AGCACACACA	GCAAGTTCT	180
CCTTCTTCC	TTTTCCACAC	CCTTACCACT	TCACTATGTT	TCTACCAATC	CAGTGCCCCAG	240
TTGCCAATGA	TGTTGCTCTC	ACATGAATT	ACTGCATTCC	CTTCTGGTTC	CCAGAAGGT	300
CTTGAAGAAA	GAGGTTCTAGA	CTAGTGGAC	CAAACAGAAAT	TTCTGGCTG	GTGATACTCA	360
GATTGTGTT	AGAGCCTGGT	ATGAAGAAGG	GGCCAGGTGT	AAGAAGTAGT	TAATCAACTG	420
CACGTTGATT	TCAGGCTGAA	TATTCAACCA	TCTGCAGCCA	CCCGCTCTA	AAAGTCTAGC	480
TGAAGCACAA	TTGATTGTGC	CATAGAATGA	GCAAACGCTT	AAAACACAA	GCTCGAG	537

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

GCGAGCTCGT	TTTTAAAGG	ACCAAATAGA	AGTTTACAG	GAGAGAAGTG	ACAGAAGTGC	60
TGTCTAGATA	GAGGAAGGGC	ACACACAGAT	GCAAGCATGT	GCAGAAATGA	GCAAACCACT	120
GAGACGCTGC	CTTGAGCTCT	GTGTACACT	GCTATGTTGC	AGCCTGGGAG	GCTGTTCCA	180
GTGGAGCCCT	TCGGAACCAAG	CCATGAGATG	GCACGGTAC	GCGGAAGGG	GCAGTCTCCA	240
TGGCTGGGTG	GTGATGGGGG	CTTCTCGAG				269

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GATGGCTCCC	CAGAGCCTGC	CTTCATCTAG	GATGGCTCCT	CTGGGCATGC	TGCTTGGGCT	60
GCTGATGGCC	GCCTGCTTC	CTTCTGCCT	CAGTCATCG	AACCTGAAGG	AGTTTGCCT	120
GACCAACCCA	GAGAAGAGCA	GCACCAAAGA	AACGGAGAGA	AAAGAAACCA	AAGCCGAGGA	180
GGAGCTGGAT	GGCGAAGTCC	TGGAGGTGTT	CCACCCGACG	CATGAGTGGC	AGGCCCTCA	240
GCCAGGGCAG	GCTGTCCCTG	CAGGATCCCA	CGTACGGCTG	AATCTTCAGA	CTGGGAAAG	300
AGAGGCAAA	CTCCAATATG	AGGACAAGTT	CCGAAATAAT	TTGAAAGGCA	AAAAGCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

GCCACAATAG CGGGATTGAT CTCCTTAGGA CCTATCTTG GCGTTGCCAG TTCTTAC	60
CTTTTGTGAG TTTAGGTTTG ATGTGCTTTG GGGCTTGAT CGGACTTGT GCTTGCATT	120
GCCGAAGCTT ATATCCCACC ATTGCCACGG GCATTCTCCA TCTCCTTGCA GGTCTGTGTA	180
CACTGGGCTC AGTAAGTTGT TATGTTGCTG GAATTGAAC ACTCCACCAG AACTAGAGC	240
TCCCTGACAA TGATCCGGT GAATTGGAT GGTCTTCTG CCTGGCAGAA CTCGAG	296

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

GAATTCCGCC TTCATGGCCT AGGATGTAGA ATCCTGCTTA TCTGTGAAAT GCAGTTGACA	60
CATCAGCTGG ACCTATTTCC CGAATGCAGG GTAAACCCCTTC TGTTATTTAA AGATGTAAAAA	120
AATGCGGGAG ACTTGAGAAG AAAGGCCATG GAAGGCACCA TCGATGGATC ACTGATAAAAT	180
CCTACAGTGA TTGTTGATCC ATTTCAAGATA CTTGTGGCAG CAAACAAAGC AGTTCACCTC	240
TACAAACTGG GAACAATGAA GACAATGAAC TCGAG	275

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

TCGTTCCCTT CATCTTTCC CTTGCCAGAG CAGGGACTCT CTCCATATAA ACAAAAGGAA	60
AACCACTGGC CAGGGTATGG TCAATACCTC AACATATCCA GACATCACAG CACCAGAAC	120
CCAGTATGTA TATTCCACAA GTACTCGAG	149

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

GCAATCAGAT AAAGAAAGAC CTGGCTGACA AGGAGACACT GGAGAACATG ATGCAGAGAC	60
ACGAGGAGGA GGCCCATGAG AAGGGCAAA TTCTCAGCGA ACAGAAGGCG ATGATCAATG	120
CTATGGATTC CAAGATCAGA TCCCTGGAAC AGAGGATTGT GGAACGTGCT GAAGCCAATA	180
AACTTGCAGC AAATAGCACT CTTTTACCC AAAGGAACAT GAAGGCCAA GAAGAGATGA	240

TTTCTGAAC T CGAG

254

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

GACAGCCTGG AAGTTGGAG ACCCTGACAC ACCCACCTTC TCACCTGGC TCTGCGTATC	60
CCCCAGCCTT GAGGGAAAGAT GAAGCCTAAA CTGATGTACC AGGAGCTGAA GGTGCGCTGCA	120
GAGGAGCCCCG CCAATGAGCT GCCCATGAAT GAGATTGAGG CGTGGAAAGGC TCGGGAAAAG	180
AAAGCCGCTT GGGCCTGCT GGTCTCTATT CTGGCGTTG TGGGCTTCGG AGCCCTGATG	240
ACTCAGCTGT TTCTATGGGA ATACGGCGAC TTGCACTCT TTGGGCCCAA CCAGCGCCCA	300
GCCCCCTGCT ATGACCCCTG CCTCGAG	327

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

GCCTGGAACC TGATTCTCCT GACCGTCTTT ACCCTGTCCA TGGCCTACCT CACTGGGATG	60
CTGTCAGCT ACTACAACAC CACCTCCGTG CTGCTGTGCC TGGGCATCAC GGCCTTGTC	120
TGCCTCTCAG TCACCGTCTT CAGCTTCCAG ACCAAGTTCG ACTTCACCTC CTGCCAGGGC	180
GTGCTCTTCG TGCTTCTCAT GACTCTTTTC TTCAGGGAC TCACTCTGGC CATCTCTTA	240
CCCTTCCAAT ATGTGCCCTG GCTCCATGCA GTTATGCGAG CACTGGGAGC GGGTGTATTT	300
ACATTGTTCC TGGCACTTGA CACCCAGTTG CTGATGGTA ACCGACGCC GCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

GCGGGCTGCA GAATGATAGA CGAGCTAAC AAAACGCTGG CCATGACCAT GCAGAGGCTG	60
GAAAGCTCTG AGCAGCGGGT CCCCTGTTCC ACTTCTTACC ACAGCTCTGG GTTGCACCTCG	120
GGTGATGGGG TCACCAAAGC AGGACCTATG GGCCTCCAG AAATAAGACA AGTGCCAAGT	180
GTTGTGATTG AATGTGATGA CAATAAAGAA AATGTGCCTC ATGAGTCAGA CTACGAAGAC	240
TCTTCTTGCC TGTATACAAG AGAAGAGGAG GAAGAGGAGG AGGACGAAGA CGACGACGAA	300
CTCGAG	306

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

AATCAATCAA CTAGGCATAT GACACAGTAG TCCATTATAA AAGAAGACAT ACATCCAGCA	60
CCATCAACTA ATTCTTAAGA TAAGTTATCT GGGAAAATTG AAGAACAAAT AAATTCAACG	120
AAATACTGTA AACTGAACGA AGACATAAAA CCAAAGAAAA CTGAGGCCAT TTCTGCCAAG	180
AAAGGAACAG CAAAGAGTAA AGATGAAAAA TATTCTAAGA TAATACCAGA AAAAGATAAT	240
TCCTACATGG ACAAAAGATGA GCATGGTCA TCCTCTGAAA GTGAAGATGA AGCGCTGGGT	300
AAATATCATG AGGCCTTATC CAGAACACAC AATTCCGGAC TACCACTCGA G	351

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

AAGTTAAAGG TATTAATAAA ATGAGTTCT CCTTAATTAA GTTAATGCTC TTTTAGCTAA	60
TAAGACTTT TCTAGAGTTA CATATTTAA TCTGTTCAT TTTTATTTTT TCCTTTGGTT	120
TTATATTTTT AAAAGCCATT ATATCCCTCC CACTGGTAAC ATACACATAC ACAGACACAC	180
ATCTATTTCA AATGAATACT TACTACTTTA TCATTTCAAG TCTTAATTGT ACT	233

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

GCGGGCGCCGC AGCAGTTCCA GGAAGGGATGT TACCTTGAC GATGACAGTG TTAATCCTGC	60
TGCTGCTCCC CACGGGTCAAG GCTGCCCAA AGGATGGAGT CACAAGGCCA GAATCTGAAG	120
TGCAGCATCA GCTCTGCCC AACCCCTTCC AGCCAGGCCA GGAGCAGCTC GGACTTCTGC	180
AGAGCTACCT AAAGGGACTA GGAAGGGACAG AAGTGCACCT GGAGCATCTG AGCCGGGAGC	240
AGGTTCTCTT CTACCTCTTT GCCCTCCATG ACTATGACCA GAGTGGACAG CTGGATGGCC	300
TGGAGCTGCT GTCCATGTTG ACAGCTGCTC TGGCCCTGAG AGCTGCCAAC TCTCCTACCA	360
CCAACCCGGT GATCTTGATA GTGGACAAAG TGCTCGAG	398

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

GAATTCCGCC	TTCATGGCCT	ACACCCAGCC	AATTTTTTG	TATTTTTAGT	AGAGACGGGG	60
TTTCACCATG	TTAGCCAGGA	TGGTCTCAT	CTCCCTGACCT	CATGATTGTC	CCGCCTCGGC	120
CTCCAAAAAA	AGAACATTT	ATATTTGAGT	GCTATTTCTT	TTGCGGCACC	AAAACTTTAT	180
AACACACTGC	CTTCTGAATT	TTTTTTTTTG	GTTCTGCTC	AGCTCATTTG	TAATCATATT	240
GTTCCCATGT	ATGTCATGAG	TTATTTTCT	CCTACTCTTT	TCAAAATTT	CTTGTCTTTG	300
ACTTTTAACA	GTTAATTGT	AACAGTGTAT	ATCTTTAAAG	TTAAATTAT	GCTTGTGAAT	360
TTTTATAAGA	GCCACAAAGG	CCTTCCTCTG	TGTTTTGTTT	TTGTTTTGTT	TTTGTGTTTC	420
ATTTTGAGA	CAGGCTCTCA	CTGTCCTCA	GTGGCTCTCG	AG		462

(2) INFORMATION FOR SEQ ID NO:287:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 281 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

TGGACAGTCT	AGAAGATGCT	GTGGTCCCCC	GGGCTCTGTA	TGAGGAGCTG	CTGCGCAACT	60
ACCAGCAGCA	ACAGGAAGAG	ATGCCACCC	TCCAGCAGGA	GCTGGAGCGG	ACTCGGAGGC	120
AGCTGGTACA	ACAGGCCAAG	AAGCTCAAGG	AGTACGGGGC	ACTTGTGTCT	GAAATGAAGG	180
AGCTCCGTGA	CCTTAACCGG	AGGCTCCAGG	ACGTGCTGCT	CCTGAGGCTT	GGCAGCGGTC	240
CCGCCATTGA	TCTGGAAAAAA	GTAAAGTCAG	AATGTCTCGA	G		281

(2) INFORMATION FOR SEQ ID NO:288:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

AATGGAACGT	CTGACACAAT	ACTCGTGTAA	CTGTGTGGAA	CCGCATAATC	CCAGCAATGG	60
CACATTGAAAG	GAATGGAGGG	AATCCAATAT	TTCTGCCCTCT	GACATAATT	GGGAGAACCT	120
AACTGTGTCA	GAATGCAAAT	CATTGCATGG	AGAGTATGTT	GGACGGGCCT	GTGGCCATGA	180
TCACCCATAT	GTTCAGATG	TTCTATTTG	GTCTGTGATC	CTGTTCTTTT	CCACAGTTAC	240
TCTGTCAGCC	ACCCCTGAAGC	AGTTCAAGAC	TAGCAGATAT	TTTCCAACCA	AGGTTCGATC	300
CATACTGAGT	GACTTTGCTG	TCTTTCTTAC	AATTCTGTGT	ATGGTTTTAA	TTGACTATGC	360
CATTGGGATC	CCATCTCCAA	AACTACAAGT	ACCAAGTGT	TTCAAGCCCA	CTAGGCTCGA	420
G						421

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

AAGCCAATGG	CTGGTCGTGA	TCCTGAATGC	CAACGCACAG	AAATGATTAA	GAAAGAAGAA	60
GAACGTTGAA	GGGCTTCAT	ACGTAGGGAA	TCTCAGCAGC	GCCGAATGAG	AGAGAAACAG	120
CACCAAGCCG	GGCTGAGGCC	CAGTTACCTG	GAACCTGATC	GATACCATGAA	GGAGGAGGAA	180
GGCGAGGAGT	CCATCAGCTT	GGCTGCCATT	AAAAACCGAT	ATAAAAGGGGG	CATTGAGAG	240
GAACGAGCCA	GAATCTATTTC	ATCAGACAGT	GATGAGGGAT	CAGAAGAAGA	TAAAGCTCAA	300
AGATTACTCA	AAGCAAAGAA	ACTTACCAAGT	GATGAGGTAA	GACCAAATT	ATTCAATTCT	360
AGGGTTTAT	CCTGTAATCA	GGAGCCAATC	GCTTGATATG	AAAAGCTCAC	ACTCGAG	417

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

CAAGCATAACA	ATCAACTCCA	AGCTCGGTAT	CACCTGAGCC	CAGGAAGTGG	AGGCTGCAGT	60
GAGCTATGAT	CAGTAAAACA	CAAGACAGGT	TCACTGGCTC	CCATCCCAAC	CCGGACCAGC	120
TCCCTAGTAT	AACAACTCAC	ATGCATGTGG	ACTATACCC	TACAGCCCTC	TTCTGTGTGT	180
TTATGTGCAT	ATATGTAGCC	ATAGGAAAAA	AAATCAAAT	CCTTGGTGT	TCTTCTTAT	240
TTTTTCAAAT	ATTTCACCTG	CCCCATTCTC	TTTCCTTCT	CCTTCTAGTA	CTCCCATTGC	300
ATGCAGTTCT	CGAG					314

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

GTGTATGTGG	GGGGTAAGTG	TGTGTGTGTG	CGTGTGCGTG	TATGTGCACG	TGTTGTGTGT	60
GTGCCCTGC	ACACGGAGAG	CCCACTCATA	CGTAGCAGAA	AATCAAATGG	CCCCAAATCA	120
GAAACATGGC	GCATGTGAGC	ATGCCACTTC	TTGTGTGCCT	GTAAGTGTTC	AGAATGTACA	180
CGGCCCTGCA	GCTCCCGAAG	GCCAGCTCTG	CTGCAACCCC	TCCTCTGTCC	AACACAGTCC	240
TCACTGGTGT	CTTTTCTCT	TCAAATCTAC	AGCATTCTG	ATCTCTGCAA	ACAATTTAAC	300
CCAAAACCAA	GTTCGGCTG	ACAAGGCTAC	ATCTTGTTC	TTGTGCGTGA	TTAGCCTCGA	360
G						361

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

GGCATTGAAT TCTAGACCTG CCTCGAGTCG ATGCACCGAA AAGGGTGAAG TAGAGAAATA	60
AAGTCTCCCC GCTGAACATAC TATGAGGTCA GAAGCCTTGC TGCTATATT CACACTGCTA	120
CACTTGTCTT GGGCTGGTTT CCCAGAAGAT TCTGAGCAA TCAGTATTTC GCATGGCAAC	180
TATACAAAAC AGTATCCGGT GTTTGTGGGC CACAAGCCAG GACCGAACAC ACTCGAG	237

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

GAATTCCGGCC TTCATGGCCT ACTTTATTTT TTTAATTATT ATTAGTATTA TTTTGAGACT	60
GAGTCTTGCT CTATCACCCCA GGCTGGAGTG CAGTGAGCTG AGACTATGCC ACCGCACTCC	120
AGCCCCGGCG ACAGAACGAG ACTCCATCTC NAAAAAAA AAAAAATCT ATGTTCATGC	180
CTTNACACCT GTTCTGAC ATAGCTGTGC AGTATATCT TCTTCTAAGC AACGACCCAG	240
TGAAGATCCA AACAAAAGTT CACAAATATG TAGTTATCCA AGGCACCTCG AG	292

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

GAATTCCGGCC TTCATGGCCT ACAATCTTT AACTTGGG GTCACAGTT TAGCCACCTT	60
TCGGGGGGTG ACTGGAGCAG TAGGAGGTGT GGGGTCTATT TATGAATATA ATAAAATGGA	120
GCTGACTGTAA CTCGAG	136

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GAATTCGGCN TTCATGGCCT AAAATAACAC ACAATTAGTA TAGAAAAATT GCAAACACAG	60
ATAAAAGTC TTTCCTGTG ATTTCTGAA TGCACCTTG AATATTCACA TCTTACTGCC	120
AAAATGAGAT TGCTTGTGT GCGCTTCTGG AATTGCTTT TTTCCAGCTT ACATGTTCTA	180
GGTCCTTCCA GATCAATAGC TGCACCTCCCT CCTTCCTCTG CTGGTTCTC AGCTCGATGG	240
GCTGTAAGTG GCATTACTCT CGAG	264

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

GAATTCGGCC TTCATGGCCT ACAACCTCAT AAATCTCATT CTTAATTTCA CTCTAGGACA	60
GAATTATGT AGCACCTGTG TTCTGTTATT TTAGATTCTAT TTTAACCTAC CTAGACACGG	120
GTACTGTGT AGTTGTAGAC GTACAGATGT TGAGTTCCA TCCTCTGGC TAAATGTCAC	180
TGGGGTATT AATAACACTTC ATAAGCATTG TAGGGACACC TGCTGTCGTC TCAACCCCCA	240
GCACAACTCGA G	251

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

GAATTCGGCC TTCATGGCCT ACATCTGGTA AATTTTTCTT TCTGCCTGAG GAACACCCCT	60
TAGCATTTAT TTAGTCTGCT GGTGACCAAT TCTCATATTT TGTTTGTCTG AAAAATACCT	120
TTATTTGTT TTAATTCTTG AAAGATATTT GCACTGGTGT GATTGGATTG ATGATTGCTT	180
ATTATTTCTT TTTCCTTTT TCTTTTTGA GACAGAGTCT CGCTGTCGCC CAGGCAGGAG	240
TGCAGTGGCC CGTACTCGAG	260

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

GCTCTGAATC TATTTCTAG GACATTTTTT TCCCATTAG ATTAAGCCAG AGAGAGCCCT	60
TTCTTGCCTC CCAAGAGTTT TTCTTTGTGT GACTGTTGGT ATTCTGAACC TCTTGGATTT	120

GATGCCGGA ATTGTCCTAG AGACTCTCCT GATTCTGTC TCATTCTTG ATTCACCCCT	180
GGGGAGCTGG GGAAGAGATA CCTTCCCATG GCATCACTTG TTAAGAGTGG ATCCCCCTTC	240
CCCCMTTCCT TCTGTCCCCC TCGAG	265

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

GAATTCCGCC TTCATGGCCT ACCAAAACAA AAGAAGAAAT CATTCACTC ATGCTTAGAA	60
AGATGTCAAG AGGATGGAGG AACTCACATTG TGTTAACTCT TCTGCCTGTA ATATATGCTT	120
TAAACACTAA AAATGATGAG CATGAATCTG CAATTCAAGC CCTCAAAGAT GCTCATGAAG	180
AAGAAATTCA ACAAAATTCTT GCTGAAACAA GAGAAAAAAAT ATTGCAAGTAT AAAAGCAAAG	240
TAACAGAGGA GCTAGACCTT AGAAGAAAGA TTCAAGTTT AGAATCATCA TTAGAAGATC	300
ACAATCTCGA G	311

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

GCGATTGAAT TCTAGACCTG CCTCGAACTC GTGGCCTCAA GTGATCCACC TGCCTCACCC	60
TCATCACCTG CCAAGTCCTA CCCATTCTAA CCCTGATAGC TCTTAAATCA GGTCCTTCCA	120
CCTCAACCTC ATTATCACTG CTCTAGAGCT CAAGCCTTCA GTGTCTTTTC ACTTCCTGAA	180
TTTACTGTCT TAGTGCTCTT GCTCACATTG TATTCTNTGC CCAAAATGCT CTTACCACTC	240
CCNTCTTTC TCGAG	255

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

GAATTCCGCC TTCATGNCTT ACTTGGATTT ATCACAGTAG CATTGTCCTT CAATCTGTGT	60
GTAACTAGA AATCAAGGAA AGACATGAGG AGATTTGTCT ACTGCAAGGT GGTTCTAGCC	120
ACTTCGCTGA TGTTGGTTCT TGTTGATGTC TTCTTACTGC TGACTTCAG TGAATGTAAC	180
AAATGTGATG ACAAGAAGGA GAGATCTCTG CTGCCTGCAT TGAGGGAGAT CCGCACCGAG	240
CTGGTGGAGC AGTTCAAATG TCTGGAGCAG CAATCAGAGT CGCCACTGCA GCTGCTCAA	300
GACCTCCAGG AGTTTTCCG CGGGAAAGCT GAGATTGAGC TCGAG	345

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

GAATTCCGCC	TTCATGGCCT	AATCCTCCAG	ATTATTATCG	ATATGAAGAT	TATTATGATT	60
ATTATGGTTA	TGATTACCAT	AACTATCGT	GTGGATATGA	AGATCCATAC	TATGGTTATG	120
AAGATTTC	AGTTGGAGCT	AGAGGAAGGG	GTGGTAGAGG	AGCAAGGGGT	GCTGCTCCAT	180
CCAGAGGTG	TGGGCTGCT	CCTCCCCGCG	GTAGAGCCGG	TTATTACACAG	AGAGGAGGTG	240
CTGGATCAGC	AAGAGGC	CGAGGTGCGA	GAGGAGGTG	CCAACAACAA	TGATCTCGAC	300

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

GAATTCCGCC	TTCATGGCCT	AAAAAAAAGA	AGTTTATTTA	AAGAAACTCT	ATAAGAGCAG	60
CTTGGATTT	ATATCTTTAG	ATCCAGAGT	TTTACTTTTC	TGGAATTAAA	TATAATTGTT	120
TGGAATTAC	TCTTTATGT	TGAATTAA	AGCGTGACTA	AAGTAGTGCT	TCTTAAGATA	180
ATTGTCATGT	GTTTTTGTTT	TGTTTTGTTT	TGTTTTTG	TGCTGAGTG	TGCTCTGTCG	240
CTCAGACTGG	AGCTCGAG					258

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

GAATTCCGCC	TTCATGGCCT	ACAATTCCGA	TAAAGTTAA	GGTCAGCTGA	TGAAGAACAC	60
TCAAACAAA	GTCGCCATT	GGAGGAGCGC	CCTACCTCAC	AGGAATAGGC	CTGCATTATT	120
AGTATACTT	CTTCATTCA	AGTATGTTAT	TCTTATGGAA	ACAACCCATG	GGAAATGTAG	180
CCTTGGCATG	ACTGTATCAA	TGGATTCA	GAGCAGTAGC	GGGGACCCCC	CCAGTCATT	240
ACGTTCCACA	GCAAGTCTCG	AG				262

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

GAATTCCGGCC	TTTCATGGCC	TAAATCTCAT	AAATAGAAAG	AAAAATAATC	TAGAAATTTT	60
TCAAAGCTAG	TACTCTTCT	CCTTATAAAT	GTACACAATT	TTAATCTTTT	TACAAATTAA	120
TTTAACGTGA	CCTACTGTAC	TTATTGTAGA	TCACATGACG	CAGTTAAGTC	ATCACCCAAG	180
GATTTATGAA	TTTGAGAGATTA	CTGACCTGTT	TCATTATGAG	TGCATTACAA	TCAATATTTG	240
TGAATTGTT	GTTCAGCTTT	TCATTCAAAC	AAAAAATATT	CCCCCAAGAA	AACTCGAG	298

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

GCGATTGAGT	TCTCCCTGCT	GGTTCTTTG	AATCACACCA	AATGAATGGC	TTGCTACTGTC	60
TCCCTCACAC	CTTCATATTG	TCCATGGTTT	TTCCCAACCTC	CTTAGCTATA	CAGCTGCTGT	120
TCCTCCTGCT	TAAAATGTCT	GAACATTCCC	TCAGTGTCA	GCTCAGCCC	CATCTTACAT	180
CTTCCCTAAG	GATGTTTTTC	TGCTGCTATC	ATTCAATTTC	TTCCCTATGAG	TTCCCTCTGTT	240
ATATTGCGCC	ACCGAAACTC	GAG				263

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

GAATTCCGGCC	TTCATGGCCT	AGCCCCGACT	AGCTTGCCC	TAACCTCTTC	ATCAAAAGAC	60
CCCCCGCCAG	CTTCCCACAC	CTCATACGCA	GCCACATCTG	CCCTATTCTC	CATGCTTTCC	120
AGCTTGCTG	CCCTTCCCTCA	TCTCTCCCTG	CCTGTGAGA	CCTCCACCCCT	TCTTCCCTCC	180
ACCCCTCCAT	CCCCCAATGC	TTGTAGACCT	TCCATTCAATT	CCGTCTCATC	GTGCGTGGTC	240
TCTGATCGTC	CATCACCTGA	CCTCGAG				267

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

GAATTCCGGCC TTCATGGCCT AGCCAAAATC ACAAGAAAAAA TAACTTTGAC TTTGAAAACA	60
AATAAGTTAG AAATGCAGTG TTTCACCTTC GTGGTTTATG TTTGCTTGG TGCCCTCTCA	120
TTCCCACTTA GCCTCAGTCT CCAGGGCCTG GGCTCCACCA AGGAAGACTC CATCTGCTCT	180
CTCTATTTGC ACACTGGAA CTTTTTCCC CAAGGTACAG GATATGATTG AGGGTTTATG	240
GATGACCTCC CACCCCTCGA G	261

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

GAATTCCGGCT TCATGGCTA CCTATTCCA AACTTTAAAT GTTGTCTACC AAATACTGAC	60
AATTATGAAA ATTCTACCAAG TAGAACACAC CTCCCCTTG AGCTCCAGAG CACATGCTTG	120
ACATTCCTCA TTAGAAAGAA TCTTGATTTC CCCTCCAGTC TAGTCTTTCA TGTTTTGTTT	180
TTCTTTGTGA GAGTCTCCCT CAGCCTGCAA TGGCGTGATC TCGGCTCACT TCAACCTCCC	240
GTCGCTCGAG	249

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

GAATTTGTTT NAAAAAAA AAAAAAAA AGGGCNGGGG GGAAAAAAA AAAAAAGAAC	60
TCCTGGAGAG GAAAATAGCA AATGTGTCTT GCCTTTGTT GCTCTCTCTC TCTTTTTTTT	120
TCTCTCGCTC TCTTCTTCTC TCTCTTCTC TCTGTTTTA AGTCAAGCAT TGGTCTCGAG	180

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

NNNANNNNNN NNNNNNNNNN NNNNNNNANN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNNN	60
ANNNNNNNNN NNNNNNNNNN NANNNNNNNN ANNNNNNNNA NNNNNNNNNAN NNNNNNNNNNN	120
NNNNNNNNNN NNNNNNNNNNA NNNNNNNNNNN NNNNNNNNNN NNNNNNNNNNA NNNNNNNNNNN	180
NNNNNNNANNN NNNNNNNNNN CNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NANNNNNNNNN	240

NNNNNNNNNA	NNNNNNNNAN	NNNNNNANAN	GNANNNNNNN	NNNNNNNNNN	300
NNANANANNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNC	CCCCTTTGTC	360
ATNGTTNTCG	TTCCCNNTCT	TCCTTGTTC	TTTTCGGCA	CAATATTCA	420
AGCATACAAT	CAACTCCAAG	NTCGGAATT	TAATTACTTC	ATGGCCTACT	480
TGGAATGTTA	TCCCTGGGGT	GTCCTGGAC	CCCACCTGCT	TTCCTTCTCT	540
CCCTACTCTC	ACTGTAATT	ATGGACCTG	CCCGCCTGCG	TGTTGTGT	600
CCTTTCTCA	CTATTGTTG	GGTGTGGGAG	GGGGTGGTTT	TTCACTGAAA	660
ACCTATAGCT	TTCTTGATGT	TCAATCAATC	AGTCACTGTG	TCCCAGACAT	720
CACAGATTGG	TACCATCTCG	AG		ATTCAATAAA	
					742

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

GCGATTGAAT	TCTAGACCCG	CCCCAGGAGC	CTCCAGCTGC	CTAACCCAGTG	60
ACAACACGAT	TTTCTACAAA	TCTACAGCAC	AACCGAGTT	GTAACCCCTG	120
AGGACCGGGT	TGGTGTACTC	TCTGTATCTC	CTCTTAAGCT	TCGTCCTCAGGG	180
TTGTCGCTG	CCAATGTCGT	CTCGCATGCC	TGGCACCTCG	CATGCACGCT	240
CACGTGCCAC	GCTGTAGCCA	CATCCTCGAG		GCCCGCATGC	
					270

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

GAATTCGGCC	TTCATGGCCT	AGTTGATGTC	CTCTCATATT	TTGTTGTTTA	60
GTGGTGGTTG	TTATTTAGGA	CTGCCTCTGC	TCTGACAGAT	GTGTCTACTC	120
GAGAGAGACT	GTGTCCTATTG	TCCCACCAGG	CTGTCAGAT	CCAAACTCCA	180
TGCACCTCTGC	CTGGCTATTG	GTTACAGTTT	ACATTCTACC	TTCTCCCAAG	240
AGGCTTGCAT	GCAATTCTCG	AG		GTATTGAGGG	
					262

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

GAATTCTAGA	CCTGCCTCTC	CTGACACGGG	CCACCAAACC	CCTTACCTGG	60
				TTCCTTGCTG	

TAAAACCTCA	CCAAATGAAG	CCAGAGTTGA	TCATGACCCCT	CTCGTGTCTG	AATCCCTTCT	120
GGGCTCCCT	CTGCCCCCTG	CAAAGCCCAC	ATGATACCA	AGAGAAGACC	TGTCCCTG	180
AGGCCAGCTG	CTTCAGCCTC	TTCCCTCACA	CACATCGTCC	CGCACACGGC	AGCCACCATG	240
GACTCAACAT	CCCCGACACA	CGGTGCTGCC	CTCTGCATGC	ACCGACCCCC	TGCCCTCCC	300
ACCAAGCTCGA	G					311

(2) INFORMATION FOR SEQ ID NO:315:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 232 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

GAATTCCGCC	TTCATGGCCT	ACCTAGGTGC	TTTTTAAAT	ATTCAGACAA	ATATCTATCT	60
TACATTGATT	AAACCCGTGT	AAATTCAATT	GCAGTATCTA	CATCGAATGT	CAAAAAAGTA	120
TACTTATTT	TGTTCCATAC	TTATGTACAA	TTTTTCCCT	CTTCAGGCTT	TTTCATTTAC	180
CTTTTGAAA	AAGCACTTAC	TCTCCCTTC	CCTATCACCC	CATCCCCTCG	AG	232

(2) INFORMATION FOR SEQ ID NO:316:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

GAATTCCGCC	TTCATGGCCT	ACAGTTGTT	ATACTTCCTT	TACAAATATA	AAGATAGCTG	60
TTTAGGATAT	TTTGTACAT	TTTTGAAAT	TTTGAAATG	CTAGTAATGT	GTTCATCACC	120
GCAAGTATT	GTGCAAAC	TAATGTCATT	TTCCCTAAAGA	TGGTTACAGC	TATGTAACCT	180
GTATTATTCT	GGACGGACAC	TCGAG				205

(2) INFORMATION FOR SEQ ID NO:317:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 299 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

GAATTCCGCC	TTCATGGCCT	AGGGCTTGTC	TTTTCATTG	TTGAGTTGCA	GGAGTTCTTT	60
ACATATTCTG	GATACTAGAC	CCTCATCAGA	TATGGTTTTA	AAATACTTTC	TCTCATTCTT	120
TTCACTTTCA	AGTATCCCTT	TGATGCACAC	ACCCAAAAAA	GCAAATAGTG	TCCATTGCA	180
TTCTTTGATG	AAGAAGAATA	CAAGCAGTAA	GTCAATTACA	GCCTATTTTT	TTCTTTCTT	240
TCTTTCTCTT	TCTCTCTCTC	TCTTTCTTC	TTTGAGGCAG	GTAGGCCATG	AAGGCCGAA	299

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

GAATTCTAGA CCTGCCTCGA GCTCCAGCTG CCAACACCCCT TGGACACAAT ATTCCAGTCT	60
CCACTGCCCA TCTCATGTGG TTCAGGTTCC TCGAG	95

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

GATGCTTGGC TCACCTCCCG CTACTGGCCC CCAGACTTTT CCACCCAGG AAATGTCTCC	60
CCTGCCTGCA GCTTCAGCGA AAGCCCAGGA GGCAGGCCAA TCACITGAG	109

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

GAATTGGCC TTCACTGGCCT ACACATTCT GTACCTGGAA AAAAATGTA TCTTATTTTT	60
GATAATGGCT CTTAAATCTT TAAACACACA CACAAAATCG TTCTTTACTT TCATTTTGAT	120
TCTTTAAAT CTGTCTAGTT GTAAGTCTAA TATGATGCA TTTAAGATGG AGTCCCTCCC	180
TCCTACTTCC CTCACCCCT TTCTCCTTTG CTTATTTTC CTACCTTCCC TTCCCTTTGT	240
CTCCCCACTC GAG	253

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

GAATTGGCC	TTCATGGCCT	AGGTTGTAAG	TGATTTATT	TTTCTTTTC	TATTTCCAG	60
TGTTCTGTA	ATGCTTCAT	ATTCCTTTG	GTAGTTAGAA	AATAAAGGCT	AATTTTAAA	120
AAGAATATCA	TAGTCTAAAA	AATTAAGGA	TGCATAGAGT	TCCCTCTTGA	CTATGTGACA	180
TCTAACTGA	ATGAACTGTC	TGCGTGGCAC	AGTGGAACAG	CGCAGTCTCA	GGATTCTGAC	240
AGATTTTGG	ATCCCAGCTC	TACCACTAAC	CTTGGGCAGG	ATTTAGTCC	CTCTGAGACC	300
TGCTTCTCG	ATTGAATTCT	AGACCTGCCT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

GAATTGGCC	TTCACCTAAA	TACTCCTCCT	TTTGTATCAT	TCAGCCTTTT	GTTTTAGTTT	60
GGTAAGTTT	AAGAAATTTC	AGCAGCAAAG	TTGTTATTCA	GTGGGCACGA	TGAACTCCAA	120
ATGCTCAAG	TTATGTATAAC	CTGTGGAGGT	CACTACTTC	CAAATIGTTC	TCTTCCTCAT	180
CTTCTCCCTT	TACCTGCACG	CCCAGGTGCG	CCAGCCGGGC	CTCGAG		226

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

GAATTAAT	AAACAAAAGG	CAGCCAAGGA	TGAAAGGATT	TAGTTCTAAG	ATGTTTCACA	60
GTTGTGATT	GTTTATTATA	ATCCTTAGTA	GTAAATTAGT	ACTAGAAGGA	TCAGGTATAT	120
CTTCCTTAAT	TCTTCCCAGG	GGAGAGAAAG	TCCCATTCT	CGAG		164

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324.

GAATTGGCC	TTCATGGCCT	AAGCCTATGT	TGATCTTGA	CTCCTGGGCT	CAANCCNTCC	60
TCCTGTCTCG	GCCTCCAAA	TTGCTGGAAAT	TATAAGCACA	TTACACAGTG	CCCAGTCTAC	120
CTACATTTG	ACAGACATAT	AATATTCCAT	GGCATGGTTA	CATTATTCA	TTAAGAATGT	180
TCCCCTTT	CTCTAAGATA	ATGCTGCCCA	TCTGTGTCTC	ACTCTGGACA	TGTAGAGTAC	240
CTGCAAAGAC	TTGGACTGCT	TGAGCAGAGG	GCCTGCTTTT	GTTTTTGTGTT	CTTCCTGCCT	300
GTTGTAACCT	GATGCTGCCA	AATGATCCTC	TTAAATGATT	GTACCCACCTT	CCCTGCCACC	360
ACCAGATTTT	AAGGATTCTC	TGTACCTCCC	AACACATGAT	GACATCATAAC	ATGAAAAGTT	420

TTGCCTGCCT GATGGAATAA TTGAGTCAAG AAATAGGATG CTAATGGCAT CTTCGCTTAC	480
CCGGTCTCCT CGAG	494

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

GAATTCGGCC TTCATGGCCT AGTTGGGTGT TGAGCTTGAA CGCTTCTTA ATTGGTGGCT	60
GCTTTAGGC CTACTATGGG TGTAAATT TTTACTCTCT CTACAAAGGT TTTCCCTAGT	120
GTCCAAAGAG CTGTTCTCT TTGGACTAAC AGTTGTCTG ATGAATAATT TCATTTCTC	180
CAAGTTTATG ACACCTGGAA CGTCAAGAAC TCGAGGTTTG TGCAATTGAG GACCGGTGG	240
CACTGTGCAG AGATCAGAGT ACTAAGAGAC AGAGATTAAG ATGGCTATCC TCGAG	295

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GAATTCGGCC TTCATGGCCT ACAAGGATAG AATTCAATTCC ACCTATATGT ACTTAGCAGG	60
GAGTATTGGT TTAACAGCTT TGCTGCCAT AGCAATCAGC AGAACGCCCTG TTCTCATGAA	120
CTTCATGATG AGAGGCTCTT GGGTACAAT TGGTGTGACC TTTGCAGCCA TGTTGGAGC	180
TGGAATGCTG GTACGATCAA TACCATATGA CCAGAGCCA GGCCCAAAGC ATCTTGCTTG	240
GTTGCTACAT TCTGGTGTGA TGGGTGCAGT GGTGGCTCT CTGACAATAT TAGGGGGTCC	300
TCTTCTCATC AGAGCTGCAT GGTACACAGC TGGCATTGTG GGAGGCCTCT CCACGTGGC	360
CATGTGTGCG CCCAGTGAA AGTTCTGAA CATGGTGCA CCCCAGGGAG TGCTCGAG	418

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

GAATTCGGCC TTCATGGCCT ACAGACATCT AATCGGAATC TTGCTCTTGT TGCCCAGGCT	60
GGAGTGTAAAT GGCACAATCT CGGCTTACTG CAACCTCTGC CTCTGGATT CAAAGTGTTC	120
TCCTGCCCTCA GCCTCCCAAG TANCTGGGAT TACAGCCCTG AAAACCACTC GCTTGCAGAG	180
CGCTGGATCA GCAATGCCCTA CTAGTTCTTC ATTCAAACAC CGGATTAAG AGCAGGAAGA	240
CTACATCCGA GATTGGACTG CTCATCGAGA AGAGATAGCC AGGATCAGCC AAGATCTTGC	300
TCTCATGCT CGGGAGATCA ACGATGTAGC AGGAGAGATA GATTCACTGAA CTTCATCAGG	360

CACTGCCCT AGTACCCACAG TAAGCACTGC TGCCACCACCC CCTGGCTCTG CCATAGACAC	420
TAGAGAAGAG TTGGTTGATC GTGTTTTGA TGAAAGCTCA ACTTCCAAAA GATTCTCCA	480
TTAGTTCAATT CCAAAACACC AGAAGGAAAC AACGGTCGAT CTGGTGATCC AAGACCTCAA	540
GCAGCAGAGC CTCCCGATCA CTTAACAAATT ACAATGCGGG AACTCGAG	588

(2) INFORMATION FOR SEQ ID NO:328:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 385 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

GAATTCCGCC TTCATGGCCT ACGACTGGGG GAAATGTCTA TTCTCCTGTG TATCTCTGGG	60
CTTTCTTGT TTTGGCTGC CTCTGCTCA GTTCTCTCT TTAGGTATT AGTAAAGCGT	120
TCATGTAATG TCATTCCTGA GGACCCAAAG TGATGCTTT TAACATGGTG AACATGGTC	180
ACTATATGTT GGGCAAAACAG TTCTGAGGGG CTACGCTGAG ACTGAGCTGA TTGTATGTGC	240
TGGAAAATGG AACGAAACTC CTGTTCCCTT TTGTGCTAT GGACTAGATC TCGGCAAAGC	300
TTGCGTTCCCT GAGCCAATAA GCCACTGGGT CGTGCAGGTT CCTCATCAAA AGAGTCCATC	360
CGGACATTGA CCTGTGCCTC TCGAG	385

(2) INFORMATION FOR SEQ ID NO:329:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

GAATTCCGCC TTCATGGCCT AGCAGTTCAC CACTGCAAAA CCACGGGCT GCGTGGAGGT	60
ATTCAATGGGA CACCGAGTGG TATCACTAGC AGCGGACTCT GCATGCTTAC TTAGAGCATA	120
AAAGGATAGC ACCCTTGGCC ATTGCGCTGAC ATGAACCTAG TTTGAAATT GCAGAGGTGT	180
GGAGAGCCAT GGATGGGTTT TATAATTAT TCTAAATGAA TCTCTGTGCT AAAGGCTGT	240
TGAAAAAAAT ATGAAGTTG ATGTTGCTTA AGTTATATGC AAATGTAAC TGTCCTTCCT	300
TCAAGATGTT TGAATGGAA TGAATGCCCT TCCCTGGGT ACCTCCCAAT ACCTACCCCTC	360
AAAAGAGCTC CACTAAGGCT TCCTTATCTT TCCTTGCCCT GCTTCCTACA CTGCTGCTGC	420
AGGTGTCCTC GGGTGATTGT GGGGAAACC ACTGTGGTTA AGCACCAACA CCAAGACTCG	480
AG	482

(2) INFORMATION FOR SEQ ID NO:330:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 532 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

GAATTCCGGCC	TTCATGGCCT	AAGGCCTTGG	TGCCCTGTGG	GTGGACTCTG	GGGAGGCCAG	60
GGGCCCAAGG	CCACCTTCTA	GGGCCTGAGG	AGCCCTCTGA	GACCTGCACA	CCCACCCAG	120
GGAGCGCCCC	TCCCTCCACC	TCTGTGCCCT	CCCAGTGA	CTCGAACCTC	TGTCGTGTTT	180
GCAGATTCA	CGCGAAGGGC	CGCCAGCCAG	TGGATTCCC	GGGCCTCAG	CCCTCTGGAG	240
TGTACGAGTT	TTGGAGAAC	CTCTTCCTCT	GTATATGCTT	TTGACTTCC	TGGACTGATG	300
TAAAAATACT	CTTTCTTTG	ACCTGTTAT	TTTTAAGACA	CGACGTGATT	GTGTCAGCTT	360
ATATTTATT	GCTGAAGTAA	ATTTTCAAAT	TTTTTATTAG	TTTTTTGGAA	TCTTTGTCTG	420
CTCATTTGG	AGTTTTGTA	ATTTGATAG	GTGTTCTT	ATGCTTGTA	TTGTTTCTT	480
AATGACTTTT	ACCTAGTTT	TTAACAAACC	CATAGTACAG	TGTACCTCG	AG	532

(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

GAATTCCGGCC	TTCATGGCCT	ACATTTTTGG	AAAAAAAAAA	ATCTACTTTG	TGTATGTGTC	60
GGGTGTGGGG	TGTGAGAGAT	ACATTCCTTT	TTNGTGCTA	AATCTCACAG	TCCACATATG	120
ACTTCCCCA	CTTGAGAATT	CTCTCTCATC	TGTGTGGCTC	CCTGCATTCT	ATAAAAATAT	180
AAATAAATAA	AATTTAAAAA	AGTATAAACG	CGGTGCCATG	AGACCTTGG	GTTGGGCAAA	240
GCCTGTGAAG	TTTGAACCGG	TAAACCGACG	AATACAAGGG	AGTGATTATT	ACAAGGCCAT	300
CCCGCTTAGC	ATCGGGGAAT	CATTTGGGA	GAGAGATTCA	ATTCATAAAA	GATGATTTC	360
AAGGGCTGTC	TCGAG					375

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GAATTCCGGCC	TTCATGGCCT	ACACCGGTC	AACTCTGCAG	GGCTGATGAT	AAACATGCCT	60
CTTCTCCCT	TGTCCTTCTC	CTCTCTAAAG	CAAGGTCA	TCTGTGCTCG	TCAGGCAGTG	120
GCAGGGGTTG	GGAGGAGGAG	AGAGGGAAAC	ACTGTGGTCA	GGCTCTGGGG	AGAGTTGACT	180
ACAGTGTAGC	TCTTGGATTA	TTTATGAATA	TTGCCCTCAG	ATTTATTTTC	ACTCTGCTCC	240
TTCCATTATC	ATCCCCAGAG	ACAACCAAGA	GCGGACTGTA	AAAAAAGACT	TCCAGACACC	300
TAGAATATAT	ATCAATAGAC	ACTGTTAAA	AGGGGAGACT	CGAG		344

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

TGGCCTAAAG	GGGGTGGGTA	CTCCGGTGGG	CTAAGGTCAG	AAGTCCCTG	TGCAGGGAGG	60
GAATGGTCCC	TTGAGAAGGA	ACAGAGGGCA	AATCCTGAAG	AGTCCTGGAG	GCCCAATGTA	120
GACAGCAGAA	GCTGGGAGCT	GACCTAGGAG	TGATCGGGGG	CCTGATCCAG	ACAGGACAGA	180
CACAGGCTGA	CACCCGGAGAG	TCCCAGGTGC	CAACATGAAC	AGTAAAGGCA	GGGGCTGACC	240
CCAAAGAAAT	CAGGGGCCCG	CAGCTGACCC	CGGAGGGTCC	CAGGTGCCGA	CCTAGACAGC	300
AAAGGCAGGG	CTGACCCCCAG	AGGGTCCCAGA	GCGCACCCAG	ACGACACAGG	CAGGGCTGAT	360
CCCGGAGGGC	CCCGCCCCGA	CCCGGACAGG	CAGTGAAGGC	ACAGGCAGGG	CTGACACTCG	420
AG						422

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

GGGAACGAAA	GATGGCGGCG	GAAACGCTGC	TGTCCAGTTT	GTTAGGACTG	CTGCTTCTGG	60
GAATCCTGTT	ACCCGCAAGT	CTGACCGGGC	GTGTCGGGAG	CCTGAACCTG	GAGGAGCTGA	120
GTGAGATGCG	TTATGGGATC	GAGATCCTGC	CGTTGCTGT	CATGGGAGGG	CAGAGCCAAT	180
CTTCGACGT	GGTGATTGTC	TCCTCTAAGT	ACAAACAGCG	CTATGAGTGT	CGCCTGCCAG	240
CTGGAGCTAT	TCACCTCCAG	CGTGAAGGG	AGGAGGAAAC	ACCTGCTTAC	CAAGGGCTG	300
GGATCCCTGA	GTTGTTGAGC	CACCTCGAG				329

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

GAATTCTGGCC	TTCATGGCCT	AAAACAGATA	ACGCTATAGA	GAAAACACTG	TTTACTGAAC	60
AGTGCTTGA	AACCAACGAGG	GTGATCAGAG	CCCCATTCG	CCTTCTAGAG	ATAAACCTGT	120
CTCCCTTCCT	GCAGAGCTAG	CTCCTCCTAT	TGCTTCTGGT	TGTCGTTTGT	CTTCAGTCTG	180
CTTCCCTGCCA	GTGCAGCAGC	TCCCTGCTAGA	TCTTGACATC	CTAGTGGCCA	GATCCCAGGG	240
GCGGTGCTGG	TCCATATCGGA	GCTCTCTGCC	TCATCTCCCA	TCCTTTTTT	CCACACTCAG	300
TGTGTATTCT	CTTGATTTC	CATAACCTGT	TCCTCCTTAC	ATCCACCTCT	CTACCTCATC	360
TCGGACCTG	CCTCGAG					377

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

GAATTCTGGCC	TTCATGGCCT	AGCAGGTCAG	GAGCCCCGGG	AAGGCCCCAGA	GGTACTCCAA	60
AGGGGGCCGG	CTGGTATCTG	AAGGCCCCCT	GCAGTTAGTC	TGTTGTTGAG	CTGTGGGCAT	120
GAACATGCCA	CAGGCAGACA	CTGTTTAGCC	AGGGTTTTAA	GAAACACGGA	GGGTCTGTG	180
GATCTGGAGT	TCATTTGTCA	GGACAGGGAT	GGGGACCCCT	CTGAAGTATT	CACTGTGGGC	240
TGAGGGTGC	TGCCACACA	ACCTCTGTGG	GAGGCATCTC	TTGCAGTGAA	GCTGTTGGTC	300
CTCAGTTCA	TGCCCACTGA	GGGTAACCA	GCCCCAGCTC	TGCACCCCCA	CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

GAATTCTAGA	CCTGCCGAG	CACAATCCCG	TGGACAGAGC	TTACTCCATC	TAACTCGTTT	60
TCAAGTCAT	GATTTTCACT	TTCACTTTTC	CTTTTTCTT	ATTATGTTGC	TTAACTTGTA	120
CAGTGGCAAC	TGAAATGCAT	TTCAAGAAATA	GGAGGTTTCG	TCCAGCACCC	TCTGCAGCCT	180
TGGTGCCTGT	AGCTCTGGAC	TTCCCTGGC	CTTCCCCTGT	GGGAGGGCCC	TGTAGACCAC	240
ATCAGGGTGG	GGTGGGGGTC	ACTTGGCAAA	AAGGGCCAG	GTCTGGTGAT	GTGGTTCCCA	300
GGATCTGGAA	CCTCTCCAC	CCCTCCTGCA	GTGGACTGA	ATTCTTCCCT	TTCATCCGAA	360
GAAACCCACT	TGCTGTTTCC	AGCCAACCTCG	AG			392

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

GCAAGATGGC	GACCGAGACG	GTGGAGCTCC	ATAAGCTAAA	GCTTGGCGAA	CTAAAGCAAG	60
AATGTCTTGC	TCGTGGTTTG	GAGACCAAGG	GAATAAAGCA	AGATCTTATC	CACAGACTCC	120
AGGCATATCT	TGAAGAACAT	GCTGAAGAGG	AGGCAAAATGA	AGAAGATGTA	CTGGGAGATG	180
AAACAGAGGA	AGAAGAAACA	AAGCCCATTG	AGCTCCCTGT	CAAAGAGGAA	GAACCCCTG	240
AAAAAACTGT	TGATGTGGCT	CTCGAG				266

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GAATTCTGGCC	TTCATGGCCT	AAACAATGAA	TAAAGCCAAG	CCAGTTCCTG	CCCCGTGGA	60
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GCTTGTAGTC AAGACATTGA ACAACTGATC AGAAAGATGT TGACTGCTGC AGCAGAGGGT	120
TGCAAGCTGC TCATGAGTAT ATAACAAGTA GCCCTAACCA AAGCATTCTC TCCCTTGGTT	180
TAATGTCCAC CCATTGAGGT GACTGCTAAA TACTAATCCA TGACTCTATC CCTTGGCATT	240
CAAACTCACA CATCCACTTA CCTGCCTCTC CAACCTCCCT GCCTCGAG	288

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

GAATTCTGGCC TTCATGGCCT AGTCTCTGCC ATGTTCTAAA CTGAAAACCT CCTAGTCAAC	60
TTCACACTTT ATTCCCTGAT CCTCAATTGG TTCCCATGTC CCGTTAGTGT TTCTTGTAAAG	120
CCTCTGCCAC CACCGCAGAT CGAACCTCTAA TCACATCTCA CCTGAATTAT GGAAAAGTCA	180
CCTCAATTCT CTCACCCATC CCAGCCTCCA CTATGGATTA ATATGCCCTAA AGCAGAGCTG	240
ACCACAAACGG TGAGAAGAAAT CTGAGAGGGGA AGCAGCAGCA AACACAAGAG TCACTGGACA	300
TGCATGCCCTC GAG	313

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

GAATTCTGGCC TTCATGGCCT AAGAAAAAAG GATAGACAAA TAGTATTTTT GTGATTTTAC	60
AGTAGCTTAA AACTATAGGA TTTTTTTTCC CCATTACTTT GCAACAACTG ATACTTTGAA	120
CCAGTTCTCT TTCTCTAACGCA TTTCTCTCCT TGAGCTTAA CCCAAATTGT CCTAGTTCTT	180
CTCTGTTGT CCCTCAGCTA TACACAGTCA CTGAGGCTCT GTGCTTGGCT TCTGTTCCCTC	240
TCTCCTCATA GGGATTCCCTC ATGTTGGAGT TCATCAAGCT CGAG	284

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

GAATTCTGGCC TTCATGGCCT ACCACGATAG ACCAGCTGTA GCTCATTCGA GCCTGTACCT	60
TGGATGAGGG GTAGCCTCCC ACTGCATCCC ATCCCTGAATA TCCTTTGCAA CTCCCCAAGA	120
GTGCTTATTT AAGTGTAAAT ATTTTTAAGA GAACTGCGAC GATTAATTGT GGATCTCCCC	180
CTGCCCCATTG CCTGCTTGAG GGGCACCACT ACTCCAGCCC AGAAGGAAAG GGGGGCAGCT	240
CAGTGGCCCC AAGAGGGAGC TGATATCATG AGGATAACAT TGGCGGGAGG GGAGTTAACT	300

GGCAGGGCAC TCGAG

315

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

GAATTGGCC	TTCATGGCCT	AAAGATGTTA	GATATTACAA	TTTGACTGAA	GAACAGAAGG	60
CGATCAAGGC	CAAGTATCG	CCAGTCATAA	GGAAAGTACGA	GTGTGAGAGA	TGACTTACAG	120
TCTCTTCTGT	TTCACTTTTT	GGATGAATGG	CTTTATAAGT	TCAGTGCTGA	TGAATTCTTC	180
ATACCCCGGG	TGGGGAGAAG	AATTTTCATT	GTCCAAGCAC	CCTCAGGGAA	CAGAAGTCAA	240
AGCAATAACA	TATTCAGCAA	TGCAGGTCTA	TAATGAAGAG	AAACCCG		286

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

GAATTGGCC	TTCATGGCCT	ACCTCTGTGA	AAATTTAATT	TTTTATATCC	TGATTAATAT	60
ATTGTGACTT	TAGGCCATT	TTTCATGTGC	TTCACTTGAA	TAGAGTTAAT	CCATAAAATT	120
GCTCTTACT	TTAGCTTATC	AAATGAAGTA	TTATTTGTG	GACTGGAGGC	CAAAAAGTCA	180
ATGTGAGCTT	CTCACAGGGT	TTTAAAGCTC	CACTAAAAT	AATTATCCAC	TTGTCTTAC	240
TTTTGTTGAC	CAGAAATAGTT	GGTAACCTCTG	CCAGAGCCTG	TACTTACCTG	CCAAAAACAA	300
TTAAATCTGG	TTAATGCCTG	AAACCAAATC	TCTCAGTCTC	AAAGTGTATA	CTATCCAAGT	360
TTTAAATGGA	AAGGTAAACT	GTGGAGTAAT	GAAATTGTTG	TTTTACTGTA	CCTTTTGCTA	420
TCAAGATAAT	ATTCATGTTT	GAAATCTTGT	CTTTATTGGA	AATTAGTTA	CTGTCTGCTT	480
TTAACCTTGTG	CTTCCCTAAA	GAAAGTTGAA	GATCCAGAGA	GTTCAAGGG	TCGGGGAGTC	540
TCGAG						545

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

GAATTGGCC	TTCATGGCCT	ACAATAAGTG	TGTTATACTT	GCTTGGGTGA	TTGCAATCAG	60
CATGGGATT	GGCCATTCT	ATGGCACAAT	TCAGATTCA	AAGCGTCAAC	AGTTAGTCAG	120
AAAGATACAT	GAAGATGAAT	TGAATGATAT	GAAGGATTAT	CTTCCCAGT	GTCAACAGGA	180
ACAAGAATCT	TTTATAGATT	ATAAGTCATT	GAAAGAAAAT	CTTCAAGGT	GTTGGACACT	240

TAATGAAAGCA GAGAAGATGT CCTTGAAAC TCAGAAAACG AACCTTGCTA CAGAACTCGA	300
G	301

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

GAATTCCGCC TTCATGGCCT ACACATTTG ACAGCTTCCT TTCAAGTTTC TTGAGCTCTC	60
AGAAAAATTG AAAGGAAGTG GGCTGGGAT ATAGAGAGAG TCCAAACTAC CAACTAATGA	120
ATGAATCTGA AGGAGACACA GAAGGGCAAG TAGAGTTAG AGTTTGAGAG TGCAGGAAAG	180
TTTGAAATG CTCAGAACTG CCAGAGTAAT TTCTGAGATC TTACTAAGCA CTCTCCACC	240
GTTTGCCTTA AAAGATACCCC TTCCCCCAA TTGAAACATC ACAAATCTGC AGAGCTCTT	300
AATCAGGTGT GTTATACACA ATGAATTAA TTCTCTTATT GCCCTGGAAG AAAGATAAAC	360
CAGATGTGGC CCTTGCCCTT TTTCAGTAAG TATTTGTTAG ATCTTCATTA CATTAGGC	420
CTCCTAGGCC ATGAAGGCCG GCCTTCA	447

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

GAATTCCGCC TTCATGGCCT AAAATTCGGC TGATTTCCCC CTTGGCTAGG CCAGCTGACG	60
GAGTCAGAG CAAACCAAGA AAAACTACAG AAGTGACAGG AACAGGTCTT GGAAGGAACA	120
GAAAGAAACT GTCTTCCTAT CCAAAGCAA TTTTACCCAG AAAAATGCTG TAATTTCTTG	180
GGAAGATTTT AATGTACACC TATTTGTAAA GTCATCAGAA TAGTGTGGAT TATTAATAT	240
CTAGTTGGA AGAAAATAAT TTATATAAT TATTGTAAAT TTTTATGTAA ACTCGAG	297

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

GAATTCCGCC TTCATGGCCT AGAATAAAAC AAAGCCTTTT CTGCCCTTTA CATTCAAGTT	60
AGTAACCGTC AACACCCAC CCATATACTC CCATACCATG AGGTGTAAATT TTCAAACCTCC	120
TCGCATACTT TTAATTACTA GTTTAATTAT TTGCTCTCTC ACTGAGTCTA TAATCTCACT	180
TAGGGTAAGA ACAGAACTCA ATTACAGATG CTCAGTAAAC ACTGGAAAGGC CGCGGCTCGA	240
G	241

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GAATTCGGCC TTCATGGCCT AGGGCTGCC AAGATTCGTA AAGGTAAGTA GTATCTTAT	60
TTGGGGTAA CTTAATTATA GATAAAAGAT GGTCCAATAC TGGAAACTGT TCGTTCTTC	120
CCTTGGATCT AGTCTTCTTC TGCTTTATAT AGAATCCAC CATCATCTCG AG	172

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

GAATTCGGCC TTCATGGCCT ACACGTGACA GCCTTTCACT TTTCAGATCA CCTTCCTCAC	60
ACTGATGGTC TCATACAACA TCATTTGAA TGTCTCAGC TCTCTGCACC ACCCACCAA	120
CTCCACTCTG GGCCACCGCT GGTGTATCCA AGATCAGGAC ACCAGTCCCT GGGCACCAGG	180
GAGTATGCTG GCCACTGAAG CAGCTCGTT TTTCCGGCAC CCATGTTGTA AAATCGACTC	240
CCCCAAACTC GAG	253

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

GAATTCGGCC TTCATGGCCT AGAAAGTTA AAGATTAGCG TACTGATTAT GATGGGATT	60
TTACTGAAAA TTAGTTTGT CAGGCTGCTT GCTTGTCTGT GTATTTCTA TTCTAATTAA	120
GTTTTTATTT TTATCAAAGC TGTTTTACT TATAATGTA AAAGTCAATT AGTTTCCAA	180
GGCTTATTAT GGAAAACAGT AGTTCCCCAG GCTCCCATCC CTATGTCCAA CAAACTCGAG	240

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GAATTCTGGCC	TTCATGGCCT	AGACCTGCCT	CTAACCTTT	GATTATTCA	CTGCCACTGC	60
CTACAGGCCT	TCTCCCATAT	TCCTTCTTC	TTGCTAAGTC	TGACTTAAAC	TAGGCTTAGG	120
CACCAACTCC	TATAGGAAGC	CTTCCTTGA	CCTGGCCCTC	TACTTTTCAC	TCACTGACTA	180
CCACTCAATT	AACTGAACGG	TGAAAGTAA	CCCACAGCTA	CGCATTCA	CAGACAAACAG	240
AATTTACTA	CTCTTCTCA	CTACTGGTT	ATATTTCTGC	AACCAGAAAA	TATCATTTCA	300
TCCCTAGTAA	CTATGGCTTC	CATCTGTTAC	TTCC			334

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

GAATTCTGGCC	TTCATGGCCT	AAATAATGACT	TGTTGGTTGA	TTGTAGATAT	TGGGCTGTTA	60
ATTGTCAGTT	CACTAGGCCA	TGAAGGCCA	AG			92

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

GAATTCAAGTT	CCTTATATAT	TCTAGTTATT	AATCCCTTAT	CAGGTGGATA	GTTTGCAGAT	60
ATCTTCTCCC	ATTCCTTCTTC	TTGTCCTTC	ACTCTGTTGA	TCGTTTCCCT	TGCTCTGCAA	120
AAGCTTGT	GCTTGAGATA	ATCCCATTG	TCTGTTTTG	CTTTGTTGC	CTATGCTTTT	180
GAGGTCTTAC	TCAAAAATT	TTTGCCAGA	CCAGTACCCCT	TGAAGCATTC	CCCCAATGGT	240
TTTTTTTTTT	AGTCATTTCA	TAGTTCAAGGT	CTTACTCGAG			280

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

GAATTCTGGCC	TCCATGGCCT	ACATAGATGG	GCACACTCAC	ACACAGAAAGT	GTGCTTGTAC	60
AATCACCA	CAACGACAAA	CACACACACA	CACTAAAAT	ATAAAACACA	TGCGTCACAT	120

GGGCATTC	GATGATCAGC	TCTGTATCTG	GTAAAGTCGG	TTGCTGGGAT	GCACCCCTGCA	180
CTAGAGCTGA	AAGGAAATTG	GACCTCCATG	CAGCCCTGAC	AGGTTGTGGG	CCCGGGCCCT	240
CCCTTGTGC	TTTGTATCTG	CAGCTCTG	GCCTTTATA	AGTCACATCCT	AGTCCCTGCT	300
GGATGCCAGG	GGGCTGGATG	GGGGGCAGGA	CTAATACTGA	GTGATTGCAG	AGTGCTTTAT	360
GAATTACACT	TATTTATCG	AAACCCATTG	GACTCGAG			398

(2) INFORMATION FOR SEQ ID NO:356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:356:

GTGTCAGAGC	AGGCATTC	CAACCTAAGG	AAATCTTGT	TTTCAAATAT	TAGGGTTTTT	60
TTTTAATTGT	GGTTAAAGGA	TTTTGGACAT	GCTTTGTAAA	TTGTTAGTAA	AAGGACCTAT	120
TTTCCACCTG	TATTCTAAGT	TATTTTTTTC	CCTCTTTTG	AATTTTCAG	GTCAGCCCTT	180
CATAAACCCA	GATGGGAGTC	CAGTTGTGA	TAATCCTCCT	ATGACTCAAC	AACCAGTTAG	240
ATCCCAAGTG	CCTGGACCTC	CACAGCCACC	TCTGCCAGCC	CCACCTCAAC	AACCAGCAGC	300
TAATCACATT	TTCTCACAGG	CGCATCTCGA	G			331

(2) INFORMATION FOR SEQ ID NO:357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:357:

GCTGCCCTCGA	GGTCTCCAAG	ACTTTTCAT	CTCGTATCGT	TTCGGGATCC	GTATCCATAC	60
TTTTTATTTC	ACTTTCTTCC	TCTTCCTCCT	CGAACTCCTC	GTCGCCATCC	TGTCTGCCCA	120
GCTTCCCGTA	GCCATCCTCG	CCTTCTTCT	CGTGCTCCTT	CTCGCTCTCG	CCATCCCTCG	180
GCATACTCTC	CCTCTTCCTC	TCGAG				205

(2) INFORMATION FOR SEQ ID NO:358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 584 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:358:

CAAAAGAGAT	GGTACCCAGCA	AGAGATTAAT	ACTAAAGAAA	TGCACTCAGA	TTTTAAAGAA	60
ACTGGAAGAA	GAGCCATTTC	TCCCAGGGAG	AAGATTCTAG	ATGTGATTGA	TGACACCATA	120
GAAATGGAGA	CAGGTCTGAA	AGCAATGGGA	AGAGAGAGTT	GCTCAAGGGAA	GAAGACGCCA	180
GAGGTGATTG	ATGCCACTGA	GGAAATAGAC	AAAGATTGG	AAGAAGCTGG	AAGAAGAGAA	240
ATATCCCCAC	AGAAAAATGG	CCCAAGGGAG	GTTAACCTC	TAGGTGAAGT	GGAGACAGAT	300

TTGAAAGCAA	CTGGATATGA	GAGTTCCCCA	ACGGAGAAGA	CACCAAGGGT	GACTGATGCC	360
ACTGAGGAAA	TAGACAAAAA	TTTGGAAAGAA	ACTGGAAGAA	AAAAAAATTC	CCCAAGGGAA	420
AATGGCCCG	AGGAGGTCAA	GCCTGTAGAT	GAATGGAGA	CAGATTGAA	CGCAACTGGA	480
AGAGAGAGTT	CTCCAAGGGA	GAAGACACCA	GAGGTGATTG	ATGCTACTGA	GGAAATAGAT	540
TTGGAAGAAA	CTGAAAGAGA	AGTATCCCCA	CAGGAAAAGT	CGAG		584

(2) INFORMATION FOR SEQ ID NO:359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:359:

GAATTCCGCC	TTCATGGCCT	ATGCTTCTG	AATTGGCAAG	ATATTCCAGG	CTTATTTGGC	60
ATTCATCTTA	CTCTAGACCT	ATTATCAACC	ATGTCTCCAA	GGATAAGTAG	ATCCTTTAA	120
GGGAAATGG	TATTTTGAAA	GCATAGTGTG	GGATCTGAGG	ATACCTATTG	CTGTCAGGTT	180
GGTTATTGTT	TGTTTCAGT	GAGTAGATCT	TGGACTTTAT	TAATTTATT	TATTTATTGTT	240
AAGAAAAGTA	CATCATGAGT	TATAAGTAAT	AATTCCAATC	CAAATTTAA	TATTGCTTAA	300
CTTCTTTGAT	TTTATATTTA	TCTTTACAC	TGAAAAGTCT	CGAG		344

(2) INFORMATION FOR SEQ ID NO:360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 362 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:360:

GCAGGTGGAC	AAAAATGAAG	CCAATGAAGA	AGGCATGCAC	TGGCCTTCA	GGTCCTGGCA	60
GTGGCAGCAA	GTCCCCCCC	GCCACCAGGG	CCAAGCTCT	GAGGGGGCGA	GGGGCTGGGG	120
AGGGTGACAA	GCCAGAGGGAG	GAGGATGACG	AGGCACAGCA	GCCGCAACCA	CAGTCCGGGC	180
CCGAAGAGGC	TGAGGAAGGG	GAGGAGGAGG	AGGCTGAGCG	GGGCCCTGGG	GCTGAAGGTC	240
CTCCACTGGA	GCTGCACCC	GGCGACCCGG	CTCCAGGCC	AGCAGAGGAC	CCCAAAGGGG	300
ATGGGGAGGC	AGGCCGCTGG	GAGCCCTCAC	TCAGCCCAA	GACAGCCCC	TTCAGTCTCG	360
AG						362

(2) INFORMATION FOR SEQ ID NO:361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:361:

GCACCAACCTC	TTGCACTGTG	AGGAGTTTAT	TGATGAATTG	AATGGGCTGC	ACATGTCCAA	60
GGACAAAGAGG	ATCAAGTCAG	GGAAGCAGTC	CAGTACCTCC	AAGCTGCTGC	GTGACAGTCG	120

AGGCCCGTCG	TTGAGAAAC	TGCCCCACAG	ACCTTCAGAT	CCTGGAAAAGA	GCAAGGGGAC	180
CTCCCATAAA	CGGAAGCGAA	TTAACCTCC	CCTGGCCAAG	CCAAAAAAAG	GGTATTCAAGG	240
CAAGCCCTCT	TCAGGAGGTG	ACAGGCCAC	CAAGACGGTG	TCTTACAGGA	CTACCCCCAG	300
TGGTTGCAA	ATAATGCCCC	TGAAAAAGTC	TCAGAACGGG	ATGGAAAATG	GGGACGCCGG	360
CTCTGTAGG	ACCTCGAG					378

(2) INFORMATION FOR SEQ ID NO:362:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:362:

GATTGTATTG	AAAGTCAGAC	ATAGGTGTGG	AACCAGTTAT	GGGAGTGAGG	ATAAGTCTAG	60
ATTTGGGAAT	CAGTCGCAGA	GAGGTGGACG	ATGAAAGTCT	GAGAAGAAAG	GATCTTGCTA	120
ATGGAGTGA	CTCAGAGCTT	GATAAAGGGA	GGATGAGTGG	AAATGGAGCT	CAACGCTGTG	180
CCTTGGGAAA	TACCTCTGTG	GATTTGGGGG	AGCACAGTGA	GAAATTCAAG	AAAGACACAG	240
ACAATGGAAT	AACCAGAGAA	CTCGAG				266

(2) INFORMATION FOR SEQ ID NO:363:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:363:

GAATTCTAGA	CCTGCCCTCGA	GCATTGCCCC	CGGCCCTAAGA	AGCTCTCTTA	TCTTGCATCT	60
TGGCTGGAC	TCCTACAACA	GCCACAACTT	CCGTGCTGGT	CTCCCAAGCTT	CTAGCCTTCC	120
CCCATCTCCT	GTGCTTTTCG	ACACAGCAGC	CAGAAGGATC	CTTTAAAAAC	AGAGGTTGAT	180
CCTGTGTTTC	CTCAAAATCC	TCCAATGCTT	TTCCTACTGC	ACTCAGAGTA	AAAGCCAGTC	240
TCTGCCCTAG	ATGCTCTGGG	ATCCTGTACC	CTCTTTGGTC	TCATGTCCTA	CAATCTGCAT	300
TCTGCCCTAG	ATGGTCTTCT	CTGCTGTTCC	TTGAACATT	CAGGAACATT	CCCCCCATAC	360
CCTCGAG						367

(2) INFORMATION FOR SEQ ID NO:364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:364:

GAATTGGGCC	TTCATGGCCT	ACTGGGTTCT	GAGAAGCAGT	GGCCCGAGCT	GAAGCATCCA	60
GACAATGAGT	GTTCAGAAGC	TGCCAGATT	TCACCTAGCC	TTAGAAGTAA	CACAGCCACA	120
TTCTGTGGT	TACAAACACA	TTTCTAAGGC	CAGTCCAGAT	TCAAACGGAG	GGCAATTAGA	180

TTTGACCCCT	TGATGAAGGA	GGGCAAGGTT	ACACTGAAAA	ACAGCATAGG	GAUTGGGAGA	240
TATTATGATG	TCCATTTTG	GAAAATCTGC	CACAGACACA	GTGAAGACAG	AGAGCCCTTC	300
TCTCTGATCG	AGGACCTCCA	GAATGATCTG	CTGAGTCACT	CAGGTATGCT	GGACCATTCA	360
CACTCACCCCC	GGAAAAGCTC	GAG				383

(2) INFORMATION FOR SEQ ID NO:365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:365:

GAGGTTCACCA	GGTTTAAGCA	TTTGTTTTA	CAAAAAGGAA	TGGGATATGG	GGGTGGTCAA	60
GTTTACGGG	TAATAACAAAC	ATTCTCTCTA	GATGGCAGGG	GGTAAGTCTG	CCTGTCCTCC	120
ATTGCTGGTA	CCACATAAGG	GATACATTAG	TAAAGTAGGG	AAAGGGTCAT	ATGTGTGGTT	180
GACCTGTTCT	TCAGAGAGGA	ACGTGGGATG	GTATCTGCTG	TGTACCTGTC	TCAGACCAAA	240
CCTGGGGGTG	GACCACTGCC	CCTTTCTCTC	CAGCCTCTT	CCACAGCCTG	ACTGTACTGC	300
CACCCGCACC	CATGAGAAGG	AGGTNNNTGAA	GGAAAGCTTGA	GGACATCCAC	CTCGAG	356

(2) INFORMATION FOR SEQ ID NO:366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:366:

GAATTCCGCC	TTCATGGCCT	ACAACCATTG	AAAAAAATATA	GACTTAGAAA	ACGAAAGTTC	60
CCCTTAATCA	CAAAGAACCA	CAGTTGACAG	GGTTGATAGA	TGTTTTTCA	GATTTTTTTT	120
TTCATATGTC	TGCTATCTT	CCCCACAGGA	ACTGGGTTT	ATTTTAGGTG	TTGTTTGCA	180
ACCTCTGTTT	TTCAAGTTGCC	AGTTTATCTC	AGACATTGTC	CTATGTCAGT	ACAGGCCAT	240
CTCGAG						246

(2) INFORMATION FOR SEQ ID NO:367:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:367:

GAATTCCGCC	TTCATGGCCT	ACAAAAAAAC	AACTTCCAG	TGGCTCTCA	CTGCTCTGAG	60
AATAAACTCC	AGGCTCTTCC	ATTGCAACCA	ACAGGATCTG	GTGATTGAC	CCCAGCCCT	120
CTTTCCAGGC	CCTCATCACC	TTGATCTCC	CTTAACCTAT	CCTGCTCCAG	CTGCACTGGC	180
TGCCTTCCTA	TTCCCTCCAGC	ATACCAAGAT	TGTTTCTGCC	ACAGGGCCGC	CACTCGAG	238

(2) INFORMATION FOR SEQ ID NO:368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:368:

GAATTCTGGCC TTCATGGCCT AGTTTTTCT ACTCCTACAA GTGTAATTG AAAATCTTT	60
ATATTAAGAA AGTAAACTGT TATGAAGCTG CTATGTACTA ATAATACCTT GCTTGCCAAA	120
GTGTTTGGGT TTGTTGTTG TTGTTGTTT TGTTGTTT TGGTCATGA ACAACAGTGT	180
CTAGAAACCC ATTTGAAAG TGGAAAATTAA TTAAGTCACC TATCACTCGA G	231

(2) INFORMATION FOR SEQ ID NO:369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:369:

GAATTCTGGCC TTCATGGCCT ACTTGGTCTT CTGCACTTTT GTCTCTGACG TACTTCCTTT	60
CTTCACAAAGT GCCATTTACA GAAAGCTGGG CTAAACCAT TCCAGCTAT TCCTCCTACA	120
GCTTCCCTGA ATTATTCAG AATACAAAAT TCTGTATCTC CAAGAAACTA TTACAGATTT	180
AGATTTAAAA ATATGCACTA TTTCCTACCT TGTATGTTT GCTTACTATT TTTTTTTGCG	240
AGAGGATATG TCTTAAAAT TGAAATGCAT CAAAAAT	277

(2) INFORMATION FOR SEQ ID NO:370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:370:

GAATTCTGGCC TTCATGGCCT ACCAAGTCAA AAAATAGAAC AGTCCGGCA CCCCAGAAGC	60
CCTTGCCAC GTGGTCACAA CCCTCCCTGT TTCCACCAAC AGTAACATTC TAGTTTTAC	120
AGTAATTCTC TCCTTGCTT TCTTGTAAT TTTACTGCCC TGTGTTCTT AATATGATTT	180
AGTTTGCCCT GGTTTGCCT TCATATAAAAT GAAATCATAC TGAATATATT ATTCATATT	240
TTGCCCAATA TTTGTTTGT AAGATTCACT CATCTTGTAG CTCCAATGTA TTTATTTCA	300
TTTTGTATA ATTATATGAT TATGCCACAG TTGTCAGTT CACTCGAG	348

(2) INFORMATION FOR SEQ ID NO:371:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:371:

GAATTCCGCC	TTCATGGCCT	AGAATTATTA	GGAAACAAAT	GGTTTGCTG	TCTTTGGTC	60
ATTAGCTTGG	CCCCATGTTT	AAGCATTCGG	TAACAACTGT	GAAGAGCCTG	CTACAAATAA	120
AGTGGTAGGT	GCTCTGAAGA	AAAATAAAGC	TGTAAAAGGG	AATAGAAAAGT	GATGAAGGCA	180
GGGGCTGTTA	GACAGGCTGG	TCAGTGTCTG	AGGAAGTAGC	CCTGCACTGA	GACCTGAAAA	240
GTAAAGAAGC	AAGCCATGGG	GAGTTGGGA	GGAGCATTCC	AGACAGAGGC	TTGATGTGTT	300
GAACCATCTT	TTCCAAGCTC	TCCTCTGTT	ACCTTCTT	TAGTCACTAT	GTCCCCTTTC	360
TATCCCAGAC	CATAATTCCA	CCATTTATCT	TAAGGCTGAG			400

(2) INFORMATION FOR SEQ ID NO:372:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:372:

GAACGATTGA	ATTCTAGACC	TGCCTCGAGA	TCAGCACTAA	CCCCCCAAAC	TCCCAGCCTT	60
TAGTTGCTG	TAGGCTGTCA	AACCAGATAA	CCAAACTGT	AAAATTGAGA	ATCAATAGGC	120
TGTACATAGG	GAECTACAACA	GAATGACGCT	CATTATTGAC	AGAATCAAGT	TCAAACCTCCT	180
TGTCCTGGCG	TCTGTTGGCC	TCTGGCAGCT	GGCTCATCTG	GCATTAGCTG	GTGACAGAG	240
TTGCTGCAAC	CCTCCCAACCC	CGCTCGAG				268

(2) INFORMATION FOR SEQ ID NO:373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:373:

GTGAGGTTTT	AACTGAGCTC	GAAGAATTGG	AATCAAAAGA	GATAGGTTTG	TCTCAGTCCA	60
GACAGTGGAT	AGCATAAGGA	AAAGTACAAC	GCAGAAAAGA	GGGGGACAGC	GAAGAGACTG	120
GATTGATGCG	TTATCTAGGC	GGTACCTGTC	TCCATTCTTT	TCTAGCCAGC	CTTGAGCAT	180
TTCATCAAGA	ATAGAGGAAT	TCAAAGTACT	GCAGTCTGCT	TGAACCACTG	CTTGTGAGTG	240
GCTCTAAAAA	AAATACTTGA	ATTGAACCTT	GAAGAACAC	TCAAATAAGG	TTTGGGGCTT	300
CTCTTTGTTT	AATACTTTAA	GCCTCTTATT	TCTAACATAA	ATATACTGAT	TGCACAGAAAT	360
TTGATTGTTT	ATAGCAGCAG	TTGCCTGTAC	TTTGAATTTC	TCAGATATTA	GAGCTGAAAG	420
ATCATCTGAG	TTACTTTATA	AATGGGGAAA	TCTCGATCTC	GAG		463

(2) INFORMATION FOR SEQ ID NO:374:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:374:

GAACGGCAGC CATTGAAGCA TATTGGAAAA GGAACCTGGGG AATTATTAA AGCACTCATG	60
AAGGAAATTC CAGCGCTGCT TCATCTTCCA GTGCTGATAA TTATGGCATT AGCCATCCTG	120
AGTTTCTGCT ATGGTGTCTGG AAAATCAGTT CATGTCTGA GACATATAGG CGGTCCCTGA	180
GAGAGAACCT CCCCAGGCAC TTCCGCCACG GGATAGAAGA CGGCAGGAGG AAATTGATTA	240
TAGACCTGAT GGTGGAGCAG GTGATGCCGA TTTCCATTAT AGGGCCAAA TGGGCCCCAC	300
TGAGCAAGGC CCTTATGCCA AAACGTATGA GGATAGAAGA GAGATTTGA GAGAGAGAGA	360
TGTTGACTTG AGATTCAGA CTGGCAACAA GAGCCCTGAA GTGCTCCGGG CATTGATGT	420
ACCAGACGCA GAGGCACGAG AGCCCCTCGA G	451

(2) INFORMATION FOR SEQ ID NO:375:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 513 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:375:

GAATTCCGGCT TCATGGCCTA CTCAGATCTT AAAATTCAAGG CTGTCAAAGA GATTTGCTAT	60
GAGGTTGCTC TCAATGACTT CAGGCACAGT CGGCAGGAGA TTGAAGCCCT GGCCATTGTC	120
AANATGAAGG AGCTTTGTGC CATGTTTGGC AAGAAAGACC CCAATGAGCG GGACTCCCTGG	180
AGGGCAGTGG CCACGGACGT CTGGGATACC GTCGGTGTTG GGGATGAGAA GATCGAAGAC	240
GTCATGGCA CTGGAAAGG CAGCAGTGT GTAGATGACC TCAAGGTTCA TATAGACAAG	300
CTGGAAGATA TTTGCAAGA AGTCAAAAG CAAAATAACA TGAAAGACCA GGAGATAAAA	360
GTCTTAAGAA ATAAAAAGCT CAAAATGGAA AAAGTCTTGC CACTGATCGG ATCTCAGGAA	420
CAGAAAAGCC CAGGAAGCCA CAAAGCAAG GAGCCTGTT GTGCTGGTGT TAGTAGCACC	480
TCTGAGAATA ATGTAAGTAA AGGAGACCTC GAG	513

(2) INFORMATION FOR SEQ ID NO:376:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:376:

CAGAATGGGA TCGAAGCCTG CCTCCTTAGG NTCTTGCCN TCATCCTCTC TGGCAAATGC	60
AGTTACAGCC CGGAGCCCGA CCAGCGGAGG ACGCTGCCCT CAGGCTGGGT GTCCCTGGC	120
CGTGGGACC CTGAGGAAGA GCTGAGTCTC ACCTTTGCC TGAGACAGCA GAATGTGGAA	180
AGACTCTCGG AGCTGGTGCA GGCTGTGTCG GATCCCAGCT CTCCCTCAATA CGGAAAATAC	240
CTGACCCCTAG AGAATGTGGC TGATCTGGTG AGGCCATCCC CACTGACCCCT CCACACGCTC	300
GAG	303

(2) INFORMATION FOR SEQ ID NO:377:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:377:

GAATTCCGCC	TTCATGGCCT	ACTTCATTGT	AAGGTACTTC	TTTGGGGCGC	TGACAGTGCT	60
CACGCTCCTG	GGCCTCCTCC	ATGGACTCGT	GCTGCTGCCT	GTGCTGCTGT	CCATCCTGGG	120
CCGCCTCCA	GAGGTGATAC	AGATGTACAA	GGAAAGCCCA	GAGATCCTGA	GTCCACCAGC	180
TCCACAGGGA	GGGGGGCTTA	GGTGGGGGGC	ATCCTCCTCC	CTGCCCCAGA	GCTTTGCCAG	240
AGTGACTACC	TCCATGACCG	TGGCCATCCA	CCCACCCCCC	CTGCCTGGTG	CCTACATCCA	300
TCCAGCCCCCT	GATGAGCCCC	CCAGGTCCCT	CGAG			334

(2) INFORMATION FOR SEQ ID NO:378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:378:

GGATTTTAAG	GATCACATTC	CAAGGGAAAC	TGATATGAAG	TTTGCATGAA	ATGTGTATGA	60
GTTATCATCA	GCTGCCGGAT	TACCTTGTGA	GATTGATCCT	GCATTGGTCG	TAGCTCTTC	120
TTCACAAAAA	TGGAAAAACA	TTAGTCCAGA	AGAACAGTAT	AAAATTGCCT	GCCTTCTCAT	180
GGTGTGGTG	CGAGTTCTT	TGCCAACACT	GGCCAGTAAT	GTGATGTCTC	AGTACAGCCC	240
TGCTATAGAA	GGGCATTGCA	ACAACATACA	TTGCTTGGCC	AAAGCCATCA	ACCAAGATTGC	300
TCGAG						305

(2) INFORMATION FOR SEQ ID NO:379:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:379:

GAATTCCGCC	TTCATGGCCT	ACCCAAACAT	TATCCCTCTA	CACTGTCCCC	ACTATGCTAT	60
ACCCCTGCAC	TATACCCCTA	TGCTGTCTCC	CTTACGCTAT	CCCCCTATGC	TATGTCCCCCT	120
ACACTATCCC	CCTTTGTTGT	CCCTCCATGC	TACTCCCTAC	GCTATCCCAC	TACTCTATCC	180
CCCTGACGCT	GTCCCCCTAC	GCTATCCCAC	TACACTGTTTC	CCCCTACACT	ATCTCCATAC	240
ACTGTCCCCC	TACACTCTCC	CCCTACTCAA	TTCCCCCTAC	ACTCTCCGCG	TACACTATCC	300
CGCTACACT	ATCCCCCGAC	GCTCTCGAG				329

(2) INFORMATION FOR SEQ ID NO:380:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:380:

GTTCGAATGC TCTTTACTTC CTTTGTGGAG CCTCCCTGCA CAAGCAGCAC	60
CATAGCAACA TGTGCAATCAA TAATTCTTTA GTCTGTAATG GTGTCCAAA	120
CCTTGGATG AAAATCATTG TAAAGAAAAG AAAAAAGCAG GAGTATTGAA	180
AAGACTCATG GAACATTAT TGGCATTACT TCAGGGATTG TCTTGGTCCT	240
TCTATTAG TACAAGTGAA ACAGCATCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:381:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:381:

GAATTCCGCC TTCATGGCCT ACATAACTCT CCACAGGCTC CCCTGGGAGG	60
CCTCACCCGC CACCTCACTT CTCAGCCCT CTTCCCATCC AAGGGCTCCC	120
CCACCCTAGT CATGATCTCG CTCCCTACT CTCTCGTAGT ACTTTATTTT	180
CTGGCTCACA TTACATGCTT ATCTTGTATT TATAGATGGT TCTACATATG	240
CATCCTTTTC TCAAAGCTCC TGTGAGGCCA GGGATGGTTT TATGCCTTTT	300
TATGTTCTAG TATAATGCTT TACACATGTT TACTCGAG	338

(2) INFORMATION FOR SEQ ID NO:382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:382:

GAATTCCGCC TTCATGGCCT ACTTTCTCTC CTTTTTCCT GTAACTGTGC	60
TTGGCTTCC TCTCATACCC GTTCTGCAT TTCACTTTT CTTCTATTG	120
TCATTTTTT TTAACCTTAT CTTTGTTC TCTTGTTAT CCCATCCTTT	180
CCATCGCAATG TGTCTCTTT TTTCTTTAT TTTCTTCCTT	240
CTCCCAAATC TTTCTTTT CACAGCATTG GAACACGGGA GGTAGTCACC	300
TGAGCGGCCT GGTGCCATC CGAGACCACT CGAG	334

(2) INFORMATION FOR SEQ ID NO:383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:383:

GCAGAAAATA	TGGTATCGGT	TTCATTTAAT	AAAAATGAAA	AAATAATTTC	CAGTTATCAG	60
TAATTCTCTCA	GTACACAAAC	CTCTGCCTTC	ATTCGCGTT	AGCCATGAAC	TTTTACTGC	120
ACAAAGGAAT	TTAAAATAGC	CAAATTCTAC	AATTCTGGCT	GGGTGTGGGG	GCTCATGCCT	180
GGGATCTAG	TAGTATGGGA	CCCCGAGGCA	GGTCTAGAAT	TCAATCCTCG	AG	232

(2) INFORMATION FOR SEQ ID NO:384:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:384:

GCCTCTGCTT	TTAATTCTATT	GGCAACTGTT	ACGATGGAAG	ACCTGATTG	ACCTGGTTC	60
CCTGAGTTCT	CTGAAGCCCG	GGCCATCATG	CTTCCAGAG	GCCTTGCCTT	TGGCTATGGG	120
CTGCTTGTC	TAGGAATGGC	CTATATTTCC	TCCCAGATGG	GACCTGTGCT	GCAGGCAGCA	180
ATCAGCATCT	TTGGCATGGT	TGGGGGACCG	CTGCTGGGAC	TCTTCTGCCT	TGGAATGTT	240
TTTCCATGTG	CTAACCCCTCC	TGGTGCTGTT	GTGGGCTGT	TGGCTGGGCT	CGTCATGGCC	300
TTCTGGATTG	GCATCGGGAG	CATCGTGACC	AGCATGGGCT	TCAGCATGCC	ACCCCTCTCCC	360
TCTAATGGGT	CCAGCTTCTC	CCTGCCCACC	AATCTAACCG	TTGCCACTGT	GACCACACTT	420
CTCGAG						426

(2) INFORMATION FOR SEQ ID NO:385:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:385:

GAATTCCGCC	TTCATGGCCT	AGGCCCTTAA	ACTGGATTCA	AAAAATGCTC	AAACATAGG	60
AATGGTTGAA	GAGGTCTTGC	AGTCTTCAGA	TGAAACTAAA	TCTCTAGAAG	AGGCACAAGA	120
ATGGCTAAAG	CAATTCTATCC	AAGGGCCACC	GGAAAGTAATT	AGAGCTTGA	AAAAATCTGT	180
TTGTTCAAGG	AGAGAGCTAT	ATTTGGAGGA	AGCATTACAG	AACGAAAGAG	ATCTTTAGG	240
AACAGTTTGG	GGTGGGCTG	CAAATTTAGA	GGCTACCTCG	AG		282

(2) INFORMATION FOR SEQ ID NO:386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:386:

GATTGAATTC TAGACCTGCC TCGAAGGCCG AGAGGGAAAG TTGAAAGGTC CCAAATTCAA	60
GATGCCCTGAG ATGAACATCA AAGCCCCAA GATCTCCATG CCTGACATTG ATCTTAACCT	120
GAAAGGACCC AAAGTGAAGG GTGATATGGA TGTGTCTCTG CCAAAGTGG AAGGTGACAT	180
GCAAGTTCCT GACTTGGATA TTAAAGGCCG CAAAGTGGAT ATTAATGCCG CAGATGTGGA	240
TGGACTCGAG	250

(2) INFORMATION FOR SEQ ID NO:387:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 344 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:387:

GAATTCTAGA CCCACCTCCA CCTTTAACTC GAAGTAACAC TCGAAATCGT TTAATGAAAA	60
CACTCTCAA ACTGAATTAA TGTGTTGATA AAACAGAGAA AGGAGAAAGT AGTAGTCCTT	120
CTCCATCAGC TGAAAAAAGGA AAGATTCTAA ATGTTTCAGT GATTGAAGAA AGTGGCAATA	180
AAAACGATCA AAAGTCTCAA AAAATTATGA AGAAGAAAGA GTCATCTTCT ATGTTGGCTA	240
CAGTTAAAGA AGAAGTCTCT GGTAGTTCAAG CAGCTGTTAC GGAGAATGCT GATAGTGATA	300
GAATTCTGA TGAAAGCAAAT AGTAATTAA ACCAAGGGCT CGAG	344

(2) INFORMATION FOR SEQ ID NO:388:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:388:

GGAGTAATCA GAGGTGTTCT TGTGTTGTA TAAGGGTGGC AGGAGTGGAC ATTCTTCACA	60
TACACCCATT ATTGTTTGA AGTGTAAAT TACCTTTTA GCTACATTTC TGCAGCTGAG	120
TTTAAATGA AAACACAAAG AGTTTTATG TTGGCTGTAC TCGAG	165

(2) INFORMATION FOR SEQ ID NO:389:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 252 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:389:

GAATTGGCC TTCATGGCT AGAACAGAGC TTACTTATTTC TTCTGAAAC CAAGGCTTCT	60
CTAGTGAGCA CCATGAGCCT TTGGAAACAA CAGATGTATA CAATAGCAAA GTTTCATTTC	120
TTTACCTTGA AACGTGAAAG TAAATCAGTG AGATCAGTGT TGCTTCTGCT TTTAATTTC	180
TTCACAGTTC AGATTTTAT GTTTTGGTT CATCACTCTT TTAAAAATGC TGTGGTTCCC	240
ATCAAACTCG AG	252

(2) INFORMATION FOR SEQ ID NO:390:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:390:

GAATTCTGGCC	TTCATGGCCT	AGGATGTTCA	CTTGCATGCC	TCTGGATTTT	AAAATTATTG	60
TTCACATGAC	TCCCTTTCTG	TGCGTGGGA	AGCAGCTACA	GAGCAGTAGA	ATCCACTGAA	120
TTGGTACACT	GAAGCAGGCA	TGCCATTAA	ATGAAGGCGAG	TTAACCTTGA	CTGTTGTATC	180
ACCAGAGTTA	AAGAATTCTG	GTGCCCTCT	TTAAGTCTTC	AGGAAGTGTG	TAGAGGCTTA	240
TTCACATTAG	TTAAACAGG	CCCCCCCCAC	CTTCCCCAAG	GCAACAGAAA	ACATAACCAT	300
TAGCTCTCTT	CCTGTTTCTC	TTCCCTCATTT	CATGCTGCT	TCGGCTGCTA	AACTGAATT	360
TTGTTACTTA	GAATATTATA	AAAGTGTGGAT	GCTTTCTATA	ATGCTATTGG	TCTAAGTGTG	420
ATTAATTTC	ATTAAGGTGT	ATAAGCCTCT	AATTATTACA	TAACTGGCAC	TGGCTCGAG	479

(2) INFORMATION FOR SEQ ID NO:391:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:391:

GAATTCTGGCC	TTCATGGCCT	AGCCTATTAC	ACAGTAAGTT	AATAATTGTG	TCCTTGCAAA	60
TAAGCATTGT	GTTCTGAAAT	GGAATCACCA	TATTCCTCA	AAAGACACT	TCCACTCATT	120
CATTAATTGA	GCAGCCCCAG	TTGATAAAAGA	ATCAGTATAT	CATGTTCTGA	TATTTAATCA	180
GCAAACATCAT	TTATTCAAGTA	GAAATTGAA	TTCCCTGTGAT	GTGCCAGGCT	TGTGAGGAGG	240
GAGACTCGAG						250

(2) INFORMATION FOR SEQ ID NO:392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:392:

GAATTCTGGCC	TTCATGGCCT	AGTCGACTCC	TGTGAGGTAT	GGTGCCTGGGT	GCAGATGCAG	60
TGTGGCTCTG	GATAGCACCT	TATGGACAGT	TGTGCCCCA	AGGAAGGATG	AGAATAGCTA	120
CTGAAGTCCT	AAAGAGCAAG	CCTAACTCAA	GCCATTGGCA	CACAGGCATT	AGACAGAAAG	180
CTGGAAGTTG	AAATGGTGGA	GTCCAACTTG	CCTGGACCAAG	CTTAATGGTT	CTGCTCCTGG	240
TAACGTTTTT	ATCCATGGAT	GACTTGCTTG	GGTATGGAGA	GTCCGCTTGA	CTACACTGTG	300
TGGAGCAGT	TTTAAAGAAG	CAAAGGAAC	CCTCGAG			337

(2) INFORMATION FOR SEQ ID NO:393:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:393:

GGGATTGAAC TCCGTGACCTC AAGTGATCTG CCCACTTGTG CCTCCAGAA CTGGGATAAA	60
AAAAAAAAAA ATAGATCCTT GGTATTATTTC CATTACATAC GGATTGTAAA ATTCACTTAA	120
ACATTCACTT CTTGGTGGGC ATTTATGTAT TTCTTTGTT TGTTTGTGTTG CAGCATTTGCT	180
CTGTTAAACC TTTTATAAG TACATCTCGA CTCGAG	216

(2) INFORMATION FOR SEQ ID NO:394:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:394:

GAATTCCGGCC TTCATGGCCT ACCACATTTG TAACGGAGCC ATTGAAGCAT ATTGGAAAAG	60
GAACCTGGGA ATTATATAAA GCACTCATGA AGGAAATTCC AGCGCTGCTT CATCTTCCAG	120
TGCTGATAAT TATGGCATTG GCCATCTGA GTTTCTGCTA TGTTGCTGGA AAATCAGTTC	180
ATGTGCTGAG ACATATAGGC GGTCTGAGA GCGAACCTCC CCAGGCACTT CGGCCTGGGA	240
TACTCGAG	248

(2) INFORMATION FOR SEQ ID NO:395:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:395:

GAATTCCGGCC TTCATGGCCT AGCCTTCCTC TACCATTTT AATTTTTTTA GACTTCATTT	60
TGTGATTTAT TGCTGCTCTG GGGGCTTCAC ATCCAATCCT TTTATGGTTT CATCTTCCCT	120
TTCCTTACAT TTGTTGCATA TAACAATGGC GTGTTAGCT ACTGCAGTGA AAAATCAATC	180
AAGCCTATTTC CATATTCAAA GGCTTGCAAT GGCACCAACG GCTCTGGAT CTCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:396:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 188 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:396:

GAATTCTGGCC TTCATGGCCT AAGTTGATCC GGATACACAC CTGCTAAAAC TGCTTAAAC	60
ATTAGAAGGA CATGCTTATG GCGTTCTTA TATTGATGG AGTCAGATG ACAACTATCT	120
TGTTGCTTGT GCCCCAGATG ACTGCTCTGA GCTTTGGCTT TGGAATGTAC AAACAGGAGT	180
CTCTCGAG	188

(2) INFORMATION FOR SEQ ID NO:397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:397:

GAATTCTGGCC TTCATGGCCT ACAGGCATGT TGAGATTGG AAAAGTGGAT GTAACTGAAA	60
TTCAGATAGC TTACTGTATT GTCTTTGTGT TGTCCTCATT TGGAGGAGCA ACAATGTGGG	120
ACTATACGT TCCATTCTA GAAATAAAAT TGAAGATCCT TCCAGTTCTT GGATTTCTAG	180
GTGGAGTAAT ATTTCTGT TCAAATTATT CCTCATGTAT CCTCCATGGT GGTGTTGGCA	240
AGAATGGATC CACTATAGCA GGCACCACTG TCTTGTCAAC TGGACTCCAC ATAGGACTAA	300
TTATTATACT GGCATAATG ATCTATAAA AGTCAGCAC TGATGTGTTT GAAAAGCATC	360
CTTGTCTTTA TATCCTAATG TTGGATGTG TCTTTGCTAA AGTCTCACAA AAATTAGTGG	420
TAGCTCACAT GACCAAAAGT GAACTATATC TTCAAGACAC TGTCTTTTG GGGCCAGGGC	480
TCGAG	485

(2) INFORMATION FOR SEQ ID NO:398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 268 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:398:

GAATTCTGGCC TTCATGCCA GTGGATCCCG AACTCTGTG GCTCTAGACT TTCAACTATT	60
TTATTTTTTC TTTGTATTT TTGTTTGTGT GCTTGCTTTT TTACAATGGG AACTAGAATG	120
TAAGATGCCA AACTCAGCCT GTGGGGAAACCA TGAGTTTCA CAACAGCAAC CACAGAGCGT	180
GGTTTCCATT TCTATTCCCT GTTCATGTGG GAGGCAGAGA AGGAAATCAG GTGCTCAGTT	240
CCAGGGACAT CACAGGACAG GACTCGAG	268

(2) INFORMATION FOR SEQ ID NO:399:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:399:

GAATTCTGGCC	TTCATGGCCT	ACACCTCTTC	TGCCAACCAG	CTGCTTGGGA	TGACTGCGAT	60
CCCGTGTGCT	TGTCTGGTA	TCTTCCTGGG	AGGTCTTTG	GTGAAGAACG	TCAGCCTGTC	120
TGCCCTGGGG	GCCATTGGAA	TGGCCATGCT	CGTCAACCTG	GTGTCCACTG	CTTGCTACGT	180
CTCCTTCCTC	TTCCTGGGCT	GCGACACTGG	CCCTGTGGCT	GGGGTTACTG	TTCCCTATGG	240
AAACAGCACA	GCACCTGGCT	CAGCCCTGGA	CCCCTACTCG	CCCAAG		286

(2) INFORMATION FOR SEQ ID NO:400:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:400:

GAATTCTGGCC	TTCATGGCCT	ACCTGCCTCG	AGATGATCAT	TCTTTTCTTG	CTTCTAGGCT	60
CTGTGTCCTC	CTGGTTTCCT	CCAACCTCTC	TGGCCTGTG	TCATTGCTG	TGGGTTCCCTT	120
TTGCCCTTCG	CACCCCTCAA	ATGGGGCTTC	TCACTCACAC	TAGTGAGTTT	TCAGTGCTTG	180
CAGACCCAAAC	ACCCCTTTT	TATAACAAAT	ATTTTTAAT	ACGTCCCTTT	CCACAACTCG	240
AG						242

(2) INFORMATION FOR SEQ ID NO:401:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:401:

GAATTCTGGCC	TTCATGGCCT	AGTCCCATCA	GAGGGAGCTG	ATGAAGAACG	GTCCCTGTAA	60
GTAAGTCACT	AGGTTCAACA	ACTGCCTGGC	CGAGCACTCA	GCCCCTGGAG	CTCAGGCCAA	120
CACCAAGAGCC	CCGGTTTAG	GGGCCAGGAG	AGCAGGTGAC	CAATTATTTG	GGGAGTCTTG	180
GGTAGAAATT	CGGCCACACA	TTCTCCCGAG	GGCTGCAGGG	GTCTCCGAG	GCAGGGCGGT	240
GGAGCAGGAT	TCAGGATGTG	GTGGGAATAG	AGTGAGGGC	AGTGGGTGGT	GCTCGAG	297

(2) INFORMATION FOR SEQ ID NO:402:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:402:

GAATTCTGGCC	TTCATGGCCT	AAAAAACTAG	AATAATGAA	GAGTAATAA	ACACAATTCT	60
TAATGTATTA	CAAGAAATAA	AAGGTTAAA	AGTAGATTT	TTAATTGAAA	AGAATTAAT	120
CAGATAAAA	TATTGAGAG	GTAATGCAA	CATTTAGTT	TGTCAAAGAA	GCTTCACAT	180
CTGGATAATA	GGAAAGAAA	AAACCAAAGC	AAAAGAAAAA	TAAGCCACAA	ACTAAAAAAT	240
GTTCAGTTCT	TGAATTAA	AAAAGTAAT	ATTGAAAGAG	CATGCTGTG	ACCTGAGATT	300

ATTTACCCAA AACTCGAG

318

(2) INFORMATION FOR SEQ ID NO:403:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:403:

GAATTCCGCC	TTCATGGCCT	AGATTGAATT	CTAGACCTGC	CTCGAGTCTG	GGCACCCCTGA	60
GCAGCAGCCT	GAGCCGGGCC	AACTCTGAGC	CCTTCGGCAT	TTCTCCGGTC	AACCGCATGT	120
ATGCCATCTG	CCGAGCTAC	CCAGGGCTGC	TGATCGTGC	CCAGAGTGTG	CAGGACAACG	180
CCCTGCAGCG	CGTGTCCCGC	TGCTATCGCC	AGAACCGCTT	CCCCGGGTC	TGCTGGCGCA	240
GGGGCGGTC	CAAGGCGGTG	CTGCTGCGCT	CTGGAGGCT	GCATGGAAA	GGTGTGTCG	300
GCCTCTTCAA	GGCCCAGAAC	GCACCTTCTC	CAGGCCAGTC	CCAGGCGGAC	TCGAG	355

(2) INFORMATION FOR SEQ ID NO:404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:404:

GAATTCCGCC	TTCATGGCCT	AGTCATGGAA	CAAGTCCTTG	CTAAACTAGA	AAACAGGACT	60
AGTATTACTG	AAACAGATGA	ACAAATGCAA	GCATATGATC	ACCTTTCAT	TGAAACACCT	120
TATGAAACCC	CACAAAGATGA	GGGTTATGAT	GGTCCACCT	GGGTGACAGA	GCGAGACTCT	180
GTCTTATAAA	AAAAAAAAAA	AAAAGAAGTG	GCAGCTCTGT	CTGCTTCTCA	CAGAGTTGCT	240
AGGGACAAC	GCTGAGGCAG	GCACCTGCC	TTGGGCTCCC	CGGGTGGGCT	GCTATTTGCC	300
TGTGGGCTCT	GCCTGCCCCG	CTGTCAGTC	CCCGGGGTGG	CTCGAG		346

(2) INFORMATION FOR SEQ ID NO:405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:405:

GCGATGAAAT	TCTAGACCTG	CCTCGAGAAC	AGGGAACTTT	CAAACAAAAG	ATATATCATA	60
GGAAAGTCAGG	TGAGAAGCTG	TCAACTGGGC	AGGCAGTGAT	GAGAATCGTA	TTGTCTTAC	120
TGTACTTTTT	TGTTTTGTTC	AAAAAACCTA	AAGCATCAGC	CATTITGAAA	GCAGAGTTTG	180
CAGAGAGCCC	CCAAACAGAGC	CAGAACCTGC	CAAGAGCGAC	TGATATTTCT	AGAATCCAC	240
GAGGCAG						247

(2) INFORMATION FOR SEQ ID NO:406:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 442 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:406:

GAATTCTGGCC	TTCATGGCCT	ACAAACATCAA	AACTCCCAAG	CAAATGGATG	AATTCAATTGA	60
GATCCAAAGT	TCAACAGGAA	CCTGGTACCA	GCGCTGGCTG	GTCAGATTCA	AGACCATTCTT	120
CAAGCAGGTC	TGGATAATG	CCCTGTACTG	TGTGATGGGG	CCCTACAGAA	TGAATACACT	180
GATTCTGGCC	GTGGTTGGT	TTGCCATGGC	ATTCAGTTAC	TATGGACTGA	CAGTTGGTT	240
TCCTGATATG	ATCCGCTATT	TTCAAGATGA	AGAACATCAA	TCTAAATGA	AGGTGTTTTT	300
TGGTGAGCAT	GTGTACGGCG	CCACAATCAA	CTTCACGATG	GAAAATCAGA	TCCACCAACA	360
TGGGCCTCGA	CCTGACTTTG	CCCCCTTGCC	CATCAGCCAT	TTGCCATCAC	CCCAAACAAAC	420
TCAGCTTCGG	GGAAAGTCTCG	AG				442

(2) INFORMATION FOR SEQ ID NO:407:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:407:

CCGAGTGACC	TTCTTGATGC	TGGCTGTTTC	TCTCACCGTT	CCCCTGCTTG	GAGCCATGAT	60
GCTGCTGGAA	TCTCCTATAG	ATCCACAGCC	TCTCAGCTTC	AAAGAACCCC	CGCTCTTGCT	120
TGGTGTCTG	CATCCAAATG	CGAAGCTCCT	CGAG			154

(2) INFORMATION FOR SEQ ID NO:408:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:408:

GAATTCTGGCC	TTCATGGCCT	AGTTTACTTC	TGCTTGATCT	TTATTCTTCC	TTGCTACTAA	60
TTTTGGATT	AGTTTGTCT	TTTCTAGACA	TTCATTGTTA	GATTGTTAT	TTACAATTCTT	120
TCTAGTTTT	TTGATGTAGA	CATTAA				146

(2) INFORMATION FOR SEQ ID NO:409:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:409:

GAATTCCGCC	TTCATGGCCT	AGATGTTGCC	AGTTTTCATG	GAGGAAGTAG	ACATGAAAGC	60
TTGTTTGTAA	TGTGTTGAC	AGAGTAGAAA	GACATTGAAG	AAGGTGATGG	TATACATCAC	120
TTGAATATTT	TTATTGAAAA	GGGAGGGAGG	AAATGGAGCG	TTAGTTGTAG	GACCAGATGA	180
TGTAAGAGA	GTTTTTAAA	GTGTACAAA	CAATGGCATG	TTGTGATACT	AATGAGAAGG	240
AGCCAATAGA	GAACAAAAAA	TTGATGATGC	AGGAGACGAC	TCGAG		285

(2) INFORMATION FOR SEQ ID NO:410:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:410:

CTCGAGGGAT	CTGGCTTCT	CTGTCCTCTC	ATTTACTACA	TNACGCTGGT	GAATTAATAG	60
ATNTCTCAAC	AAAAGGACAT	TTAAATCAAC	ATATGACACC	TGTTTAAATT	CTTAAGAACG	120
CATTAATTAC	ACATTCTAA	GAAAATGAGC	TATGACACAA	CTCTTCTCAC	TGTATAACTC	180
CTATCTGTGA	TTCTCAATCA	GGTGACTTT	CAGCTNCAG	ACGGATCTTT	TCTATTCTAC	240
TCCTCTGGTT	CGGACCAATT	AAATGNTTC	TTTGCAATC	ANACATCTC	ANNTGCCAAA	300
TCTTCAAAAG	CAAAGGAGTT	NGTTAGAAC	ATATTAGGCC	ATGAAGGCCG	AATTC	355

(2) INFORMATION FOR SEQ ID NO:411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:411:

GAATTCTAGA	CCTGCCCTCG	TATGTTGCTT	TAGCCAGGAT	TCAGAGCTAA	AGTGTAAAGTG	60
TGTGCTTCTG	CTTCTGGAT	GTATCTCTCA	AAATTGCTCT	GTCTGTTTAT	TCAGCTCCTG	120
GATCTACCTT	CTCTTTCTT	TGAATTGGAC	ACCATTCTATG	TCATTGCTCA	CTCAGAACTT	180
CAGCTGTTCT	CATGATCACA	TGCTTTCTTC	CCTGTTATG	TCCAAT		226

(2) INFORMATION FOR SEQ ID NO:412:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:412:

GAATTGGGCC TTCAATGGCCT AGTCTGCTGC TTAGCTTGTA TTTTCAGTTT AATATATTG	60
TGATCATTAA CAAAACAGCG AAGTGAATAA TGGGCATAAA TTTTCCTAAG AAGAACATT	120
TTCCACTACTT ATTTTCAAT ATTATCAAAA AGTATGTAAT TTTGGGGGGT TTTTGGTTT	180
TTTTTTTTT TGAAACAGAA TCCTGCTCTG TTCTCGAG	218

(2) INFORMATION FOR SEQ ID NO:413:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:413:

GAATTGGGCC TTCAATGGCCT ACTTTGAACA ATTGGGCATG AATTGAAACC AGGTTTCCT	60
GTTGAAAGTT ATAGCTTGAT TGGGAGATAG AAGTTGAATT GAGTTCTTC TTGCAACTCT	120
TAGTGTATAT TTTTATATCT CAGTAAGACG AGGATACCTT CAGTTGAAT CTGCATAATG	180
TTCACTGCCA AACTCCTTCT CATTAAATGC TTATGGCCTT CACATTTCTG TATAATAAAG	240
ATCAATTATC AGCACTCGAG	260

(2) INFORMATION FOR SEQ ID NO:414:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:414:

GAATTGGGCC TTCAATGGCCT AAGCATATGA ATTTGGAGA GACAGACATA CAGACCATAA	60
CAGTTCTATT TTCTATAACT ATAGTAGAAT ATCGAAATGA GAACATTGAC ATTGGTAAAA	120
GGTGTATGTA TAGTTTATAT GTTATCTTAT CAAAAGGGTA GATTACAGA ACCAACACAA	180
GTAAGCTATA GAACTAGCCC ATTACCACAA AGATCTCCC CAAGCTACAG CTTTACAGTC	240
ATACCCACCC GGCTCGAG	258

(2) INFORMATION FOR SEQ ID NO:415:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:415:

GAGGACCTTT ATAATCTACT ACTAATTACT GTGAAAGTAA ACATTGTTA ATATACCACT	60
TCTTAAAGAA ATATTTGTC TAGTCATTAA TATTCTAGTT CATCTCAAAG CTTCCATTG	120
ACAATTTAAA ATTACTAAA TTATAATATT AAAGGAAACA GTTTCTGA TTCTCATGAA	180
AGTTCCATT TGCACTGAAG ATGACTAAAC CTTTAGTCA TAGTTTAGA AGAATTGGCT	240
TTTTATAGC CATTATTTT ACATATGGGT ACGGACTCGA G	281

(2) INFORMATION FOR SEQ ID NO:416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:416:

GAATTCCGGCC TTCACTGGCCT ACTCAGAAAA GAAAATGAAA ATACCTCTAC ATGTGGTCTT	60
CCTGCTAATC TCTCTGACCT TCCTTATTCAAC CACCCCTCCCC ACTGCCCACT TACTCGAG	118

(2) INFORMATION FOR SEQ ID NO:417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:417:

GCGAGGATGG CATGGACGCT TATCGAGCAG CTTCAGGGTG GCAGCTACAA GAAGATTGGC	60
TACTATGACA GCACCAAGGA TGATCTTCC TGGTCCAAAA CAGATAAATG GATTGGAGGG	120
TCCCCCCCAG CTGACCAGAC CCTGGTCATC AAGACATTCC GCTTCCTGTC ACAGAAACTC	180
TTTATCTCCG TCTCAGTTCT CTCCAGCCTG GGCATTGTCC TAGCTGTTGT CTGTCTGTCC	240
TTAACATCT ACAACTCACA TGTCCGTCTC GAG	273

(2) INFORMATION FOR SEQ ID NO:418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:418:

GAATTCCGGCC TTCACTGGCCT AAGCAGTTGC TAATGCCAGC AGTACATAAA TTGAGGATGG	60
AGCAAAAGGA TCGACACCCAC CAATGGCTGC ATTGTGATAG GTGTGGACAG AGCCTGCCAG	120
AATTAACACAC ACGCCAGGAC TCGAG	145

(2) INFORMATION FOR SEQ ID NO:419:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:419:

GGATTCCGGCC	TTCATGGCCT	AGTGTATA	ATTAATCCIT	TAATATTATG	GTTATTAACC	60
TCTTAAACAT	GAATGAATT	TTGATTGTTT	TAACACAGTA	CCTAAGACTA	ATGCTTTCTG	120
TGGACACCAC	TGAGCTCTGC	CTCAACTCCA	CCCTCTGCGA	CCGGAGGACT	ATGCCCCTAG	180
TAACTGCTGT	CGGTGTGGAC	GCTGTGCTGG	TTCTGTTTC	AAAGGAGCA	GAAGGACAGG	240
TCTCTGAGAC	AGGATCGTTG	TCCCTACAGG	AGGAACAGTG	GCCACTCGAG		290

(2) INFORMATION FOR SEQ ID NO:420:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:420:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCCT	CCCAAAGTGC	TGTGATTACA	GGAGTGAGCT	60
GCCACGCCCA	GCCTACAAGT	TTTTCTTTAA	CTACTGTTT	AGTCACCAT	ATCCTCTAGC	120
TTCTGATATT	TTCAATTGTTT	GTGTCATTT	TCTAGATATT	CAACAATTTC	AAATTAGATT	180
TTCTCTTCGA	CTAAAGTGGA	AGAAATTTTT	CCCGTTTATT	TTCTACATGC	TAAGGATTIT	240
TATTTCATT	TTGTTATTAA	TTTCTAGTGT	TACCGTATTG	TCATTAGAAA	ATATGGGCTG	300
					GCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 301 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:421:

GAATTCTGAA	AATATTAAGA	TTTATCCTAG	CACTTACGTT	CAACATACCA	TAATTTTAT	60
ACTTCTCCAT	CTAAATAAAA	CCAAGTTTGT	TCCTACACTA	GTCCAGCCTG	CATTCTCAAG	120
AACTCCAGTG	ATTATACATC	AACATCTAGA	GATCAGGTAT	CCCAATCCTT	TCTTCCCTATA	180
TCTAAGCTAA	CTCCCTCTTA	GCCAAATGGT	ACCCTTGAT	TTTGTGTTAA	TCCTTTCCCTT	240
CCCTCCACTC	TTAACCCCTC	TCATTCCATC	TTCTCCCTCC	CTTTCCACC	CCACTCTCGA	300
G						301

(2) INFORMATION FOR SEQ ID NO:422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:422:

GAATTCCGCC	TTCATGGCCT	AGGTAAAGT	TGTCTGGTAA	TAAGGTGGAG	TGGATTTGGG	60
GCAGGTTTA	TGTTTGTGTG	CTTCTCTAG	AAGTCAAAGA	GTTGGTGAGG	TAACTGCAAT	120
CCTGTCTATA	TCAGTGTAGT	GATAATGCAC	TAGTGTAATG	AAGAATGGAG	CTGCACGTGT	180
GAGGTTTTA	AAAGTCCACAA	AGATCAGGT	TTGTCTACGG	TCAATAAAGA	TTTTTTAAA	240
AAACCCCTTT	AACTAAAGAG	AGGTAACATC	CTTTTCAAAA	CTCTGAAATT	TACATGTGT	300
GACTTATAAT	ATGTGTGATC	CTCGCTGCTT	TTCTGATCCC	TGGTGGTTGG	GGTGTGTGTG	360
TGTGTGTGTC	TGTGTGATGG	GCTCTCGAG				389

(2) INFORMATION FOR SEQ ID NO:423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:423:

GAATTCCGCC	TTCATGGCCT	AATCTTAAGT	GTTTTACATG	CTCTACCTGC	CGGAATCGCC	60
TGGTCCGGG	AGATCGGTT	CACTACATCA	ATGGCAGTTT	ATTTTGTGAA	CATGATAGAC	120
CTACAGCTCT	CATCAATGGC	CATTGAAATT	CACTTCAGAG	CAATCCACTA	CTGCCAGACC	180
AGAAGGTCT	CTAAAAGGTC	AGAGTAATGC	AGAATGCGTG	CCTTCATCTC	AGATTGTTTC	240
ATCACAGGTG	GATCCCATGT	GTCCTCAGTA	GACAAGTCAC	CTTTGTAGCT	AGCACCAAGTG	300
CCAGCTCCAT	GCCATTGAC	CTCGAG				326

(2) INFORMATION FOR SEQ ID NO:424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:424:

GCGATTGAAT	TCTAGACCTG	CCTCGAGCCA	ATCATTTTA	AATCTAATCT	GAACCTTAAC	60
TGGTTAGTTG	AGTGCATTTT	TATGTGTACT	GATGTATTTG	CATTATTCC	TTACCACCTT	120
ATTTTGTGCT	TTTATGTTT	TTTCTTCCA	CTCTTTTTT	TTCTTTGGA	ATCTCGAG	178

(2) INFORMATION FOR SEQ ID NO:425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:425:

GAATTCCGCC	TTCATGTACA	TAGATCTTCC	TAGTGTCAATT	GACAAAGGTG	ACATTTGCAA	60
GGCTTTTCT	TCATCAGATG	CAGGGATCTG	GACTTCATGT	GTATCCTTTT	ATCCACTCCT	120
CCTCGAG						127

(2) INFORMATION FOR SEQ ID NO:426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:426:

GAATTGGCC TTCATGGCCT AGAATTAAAT TGCAGAAAAT TATTCAATT CTTATAATCC	60
TTTTAATGTC TATAGGATTT ATGATGATAT CTCCCCCTTC ATCCTGATT TTTCAAGTTT	120
TTGTTTTTC TTTTTCTTA TAAATTCTGG TAAATGTTA TAAATTTAT TCATTTTAA	180
AAAGAACAG CTTTGGTTT CATAAAAGTT TATAAATTTC TTGTTTCAC TTTCATTAAT	240
TCTACTCTT ATTATTCCT TCATTTGTT TACTTGGGT TTGTTTGCC ATTTCATTC	300
TAGTTCTTA AGGTGCCAGC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:427:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:427:

GAATTGGCC TTCATGGCCT AGGCACACAG GGCGGGCAGC AACATAAACG GCACCCATTA	60
AAAAGCAAGA CTCGCTCTG AGACTAAAGG AGAAGTTACC TAAATTCTG TATAAACTCA	120
GTAATTCAATT CACTTTACTA GTATTACATT TATGAAATTC ACCTTTGTGG AAAAAGGAGC	180
GGGAGAGGGA TAAGAAAATG CCTGTTCTA GAAAACGCTC GAG	223

(2) INFORMATION FOR SEQ ID NO:428:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:428:

GAATTGGCC TTCATGGCCT AAATTCAACAGAAGACCTT ATTGTGATAA AGTTCAACGG	60
TATAGGTAAA CAACAACAAA AAAACTATCA ACCATAATT TTTCACCCCA CCAACATTCT	120
CTGAACCTTT CAGTAATATT TTATACACAT GTGCAATTTC TGCCCTTTTC ATTACTATA	180
TCATAAACTT CTTCTAGAT CATTATTTT CTGCTGCATT TTTTCAGGAT TTATCACCTT	240
TATTTTGTAGT TTTAGTTTT GTGAGTGTAC TCTCGAG	277

(2) INFORMATION FOR SEQ ID NO:429:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:429:

AAATGAGCCC TATCACTGAG AAATACGTGT TTCACTGATT AACTCTGTGT GTGTGTGTGT	60
GTGTATTTTT TTTTGGTTG TCTTCAGCTG ACAGTATGAA AAATGAAACT GCTGAAAAG	120
CTGAGCACCT GCTCACCCCTT GGCCCTCCAT TGCTTTGCC TTCACTAAAA AGCAGCCTCC	180
CTTCTAGGTC AGGAAACCAT GCCATTGAGA CTAGAACGG GCGTTCTGGG CACAGTCCCA	240
CTGTGCACAG GTTGAGAGG ACAAGTTCAT CAGAAGGAAG GCAGTCCTTA GAAGTCACAT	300
ACGTTGAGCC CCTCGAG	317

(2) INFORMATION FOR SEQ ID NO:430:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:430:

GAATTCCGCC TTCATGGCCT ACATTCAGAA AACAGAAAAG TTTCAAGAAG CAGGAAGAAA	60
AGACTCACCT ATGATCCCAA CACCCAGAGG TAATAATTAA CCATTTTGG TGTATCTCT	120
TTGTCTTTTC CTATGTGTTG CCTTATGTAG ATATGTAACA GGTTGTTGGTT TAAACCGAAG	180
CTATACCCAT TGTTGGAGT CAGGCAGGTG CGATAAATTG GTAGGTGGCT CACCAGAAAT	240
CTATTGCAAT GATGAACCTA CAGGACTCGA G	271

(2) INFORMATION FOR SEQ ID NO:431:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:431:

GAATCATTTC TGGTCACCAA TCTCTCATAT ACCACTACTG GATATTTACA ACATGCTTCA	60
GTGGAGGAGA AGACACTGCT GCTTTGAAAG GATGACCTGG AATGCCAAA GGTCTCTGTT	120
CCGCACATCAT CTATTGGAG TACTTTCTCT AGTGTCTCTT TTGCTATGT TTTGTTTTT	180
CAATCATCAT GACTGGCTGC CAGGCAGAGC TGGATTCAAA GAAAACCCCTG TGACATACAC	240
TTTCCGAGGA TTTCGGTCAA CAAAAAGTGA GACAAACCAC AGCTCCCTTC GGAACATTG	300
GAAAGAAACA GTCCCTCAAAC CCCTGAGGCC TCAAACAGCA ACTCTCGAG	349

(2) INFORMATION FOR SEQ ID NO:432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:432:

GAATTGGCC	TTCATGGCCT	ACCTGGATT	CTCAATTAT	TAAGTTGTAC	TTACCTGATG	60
CTGATGATGA	TTACTGTATT	TACACATTGT	CTCAGAGCTC	ACTCTTGC	AGGTTGTGGC	120
CTCGAAAATG	CCTTGTGTC	CCTCTGGAA	CTGTC	AGCTTCATCT	CCTCCTCCTC	180
ACCTCTGCT	GTGGTGCACA	GATACCTATA	GGCAGGCTCC	ATCTCCTCCT	CCCCAGCTCC	240
TCCCCTAGTG	CACACCTCGA	G				261

(2) INFORMATION FOR SEQ ID NO:433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:433:

GAATTCTAGA	CCTGCCTCGA	GTCCTACGGG	AAACCTCCAG	GGTTTTAGGA	AGCTGACGAT	60
GCAAGTTTAT	CCAAATGGGA	ATGATAATAA	TCATGTTTAT	TATCCTGGGG	TGCTTTCTCC	120
ATAGCAAGTA	CTCACTTAGG	TCCTGTTCAT	TAGTCAGTCT	TTTAATCTGT	ACTGAAATAG	180
GTGCTGTCGC	ATCCATGGGG	AATGAACTCG	AG			212

(2) INFORMATION FOR SEQ ID NO:434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:434:

GGTTGCAGTG	AGCTGAGATC	GCACCACTGC	ACTCCAGCCT	GGGCAACAGA	GTGAGACTTC	60
ATCTCCAAA	AAAAAAA	AAAAAAAAGA	CAACCAAC	AAAAACGAAA	CACCACCACC	120
AAAAAAAGTT	ACTGGTAGAG	TCTCCTCTAG	ATTGTTTCT	TTTCAAACT	TGTTTCATAT	180
TCTCCAACTG	CCCTCGTCCC	ATAATGTTGG	CTGTGCTTTT	CTTTGTGCTT	ACAGCTCATT	240
GCTGGGATGG	ATATGGTGAG	TTTCATGTA	CATTGACCAA	ATACAATCTC	GAG	293

(2) INFORMATION FOR SEQ ID NO:435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:435:

GAATTGGCC	TTCATGGCCT	AGGCTTGAAA	GGAAATGAGG	GAAATTCAG	TGAGTTTGAG	60
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GAATGGCAGA CTGGGTATGT GACAAATGAG TGGGTAATAA AGGAAATCTC AGATTGAGAA	120
TCCTGGCAGA TCTTCAATG GGTTAGACTC CAGGAATATT GATTTAAAG CCAGACTGAA	180
GCAAATCTA GTGATAAAGG AAGGGGAAAG GGTGGCTGAA TCAAATGTTT TACCAATACT	240
CCTTTTTTA GTATTTGAGT TAAAATTAG ATTANATGCT TGGCTTAGAA GAATGCAAAG	300
CTTCACTGAG CCTAATAATA TGGATCCCAG TGGGTGAGTG GAGGTGAGTT CACTCGAG	358

(2) INFORMATION FOR SEQ ID NO:436:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:436:

GCTCGAGAGA GCTTTTTTTT TTTTTTTAA ACATTGTATC ATTAATTAT CACGTGTATC	60
CAAGCTCTT TGAGTTTCCC TGCCCCCATC CCTGTGTATC TCCAGCCATA TCCAGCTACT	120
CCTTCCATGC TTCCCCCATT CTGTTTCTG ACTCTATTAC TCCCAGTCCA AATCTTGCTC	180
TTCACTGTCT GCACCTTGTC CTCTCCTCTC TCTAAAAAA TCTACCCAAA TTCCACCCCT	240
CTTCACAGGC CCCTCGAG	258

(2) INFORMATION FOR SEQ ID NO:437:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:437:

CAAGCCGGCC ATATTAGAGA GATGGAAATA AAGCTTCCTT AATGTTGTAT ATGTCTTGA	60
AGTACATCGG TGCACTTTTT TTTAGCATCC AACCAATTCTT CCCTGTAGT TCTGGCCCC	120
TCAAATCACC CTCTCCCGTA GCCCACCCGA CTAACATCTC AGTCTCTGAA AATGCACAGA	180
GATGCCCTGGC TACCTCGCCC TGCCTTCAGC CTCACGGGGC TCAGTCTCTT TTCTCTTIG	240
GTGCCACCAAG GACGGAGCAT GGAGGTACACA GTACCTGCCA CCCTAACGT CCACTCGAG	299

(2) INFORMATION FOR SEQ ID NO:438:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:438:

GAATTCCCTAC TAAATAATAT TAAGCAGGAA TTTTTAGGT GTTGCTTTT AGCTCCCTTT	60
TATCAGTTCT GGGAAAGCAAA CAGTGTGCA TCTCCTTGC TCTCATAGAA TTCTGTAATT	120
TTTATACAC AGGTCTCTGC TAAAAGGCAGG CATGTGTTA GAAATTCTAA AAATGAGGGC	180
TCTGAACCTT GTAATGTCC TGATACGTTT TCCCTTTTT AATCCCAACC CCCTCGAG	238

(2) INFORMATION FOR SEQ ID NO:439:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:439:

GAATTGGCC	TTCATGGCCT	ACAACTTGCA	CTTCGGCTCCA	GCATCACTGG	CCTCCCTGCTG	60
TTATTTAGGT	ATACTAGGCA	TTTCCTGTTT	TAGGGCCTTT	GTACCTCCAG	TTCCCTCTGT	120
TTGGAATGCT	TTTCCCCAGA	TAGCCCTGTG	GTAAATCTC	TTACTTCCTT	TGGGTCTGTG	180
CTCAGATGTT	ACTTTCTAG	AGGGTCCCCA	AAGCCCCCAT	GCACCTCGAG		229

(2) INFORMATION FOR SEQ ID NO:440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:440:

GAATTGGCC	TTCATGGCCT	AGAGTCTATT	AACTATTTT	CTGTTATACC	CTGCCAGAAA	60
AGAATTTAA	AAGTTAGTTT	ATGTTTTGTG	TAACCATGTT	CTTCAGAATG	CAGGTATGTG	120
AGCATCATGG	TTTCTGGGTA	ATTCTGCTGC	TCCTGTCCTT	GAAAATGGAG	ATACCACTTG	180
CAGTTTATCC	CACTGCTGAG	TATTCCAGCA	TTGGTAGTGG	TTTCACTCCA	TTGCATCCAT	240
CCAGAACTTT	CACACAGGCC	TCCCCATTAC	CCAGCATCCT	CGAG		284

(2) INFORMATION FOR SEQ ID NO:441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:441:

GAATTGGCC	TTCATGGCCT	AATAAAATAA	AAATTGGAAG	AATGGCATTT	TATTACAGTA	60
TAGTTAAGAG	ATGGCTAAG	GCAGTAAATA	AAACTTAGAA	ATGCTCAAAT	TTATTGTAAG	120
TTGCTTTAT	AATCATTGAT	ATATAAAGCA	TGCTACTGCT	AATCAATTAG	TTTTATGTAT	180
TAAGACCTAT	CAGCATGTCT	TTTTTTAGT	ATCTGGTTGA	CTTAAACATG	ATGTTCTCTG	240
TACCAATTAA	CATTTTCAAG	ACATATTCTC	CCCAAACTCG	AG		282

(2) INFORMATION FOR SEQ ID NO:442:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:442:

GAATTCCGGCC	TTCATGGCCT	ACTCACCTGC	AATCTATTGT	TTATATTGTT	GCTATGTATC	60
TCTATTCTTT	CTGCATCAAA	TAATGAATAG	CTCATTTGT	GTTGCCCTCA	AGTATGACAA	120
ATTCCCTTCC	AAATGTGATT	CCAGACAGTA	TATCCAAACA	TGTCTTTCTT	TTCCCATTC	180
TGATCATCCT	ACATGTCAAG	CACTGCCAAC	GTTTACTCAA	GAAAGCTTGG	TTAGAACCCA	240
G						241

(2) INFORMATION FOR SEQ ID NO:443:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:443:

GCAAGCACAA	ATCTAACCAT	GAGCTTCAGC	AATCAGCTCA	ATACAGTGCA	CAATCAGGCC	60
AGTGTCTAG	CTTCCAGTTTC	TACTGCAGCA	GCTGCTACTC	TTTCTCTGGC	TAATTCAGAT	120
GTCTCACTAC	TAAACTACCA	GTCAGCTTGT	TACCCATCAT	CTGCTGCACC	AGTTCCCTGGA	180
GTTGCCAGC	AGGGTGTTC	CTTGCAGCCT	GGAACCACCC	AGATTGACAC	TCAGACAGAT	240
CCTCTCGAG						249

(2) INFORMATION FOR SEQ ID NO:444:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:444:

GAATTCCGGCC	TTCATGGCCT	AGGGATTTTT	TTTCTTTTTT	TTCCTCATAT	GTGAAGTAAT	60
AGTCCTTCA	CAACAGAAGA	AGCCACAAAA	CTAAACTTAT	TGCTCACTGA	ATTTTCTTCA	120
AGGTACGTA	CCTCTTTGGT	ATTTAAATC	TAGATTATGT	TGATTTTTAT	ATTTTGTTC	180
TCATTTTCT	ATTTCTTGT	TTTCTTACT	GCAAATGGGC	TCGAG		225

(2) INFORMATION FOR SEQ ID NO:445:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:445:

GAATTGGGCC TTTCATGGCCT AGTTTGGAG AGCTCTACCT ACTAGCTGGT TATTTCTTAC	60
ATTAATTAA TACCTTTAAA AAGTATTATG AAAATAACAC ACTCAGTAA AGAAATTTA	120
AAAACAAAT GCAATAAAA TGTTGTTCTT TTCAACCTTT GACTTGTAC CTCCTCCAGC	180
TTTTCCCTTA TTAACTGTG AGAGGTATTG TCTATTAGCA GTTACTTATC CCCTTCCTCA	240
AACTCGAG	248

(2) INFORMATION FOR SEQ ID NO:446:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:446:

GGATTGAATT CTAGACCTGC CTCGAGCGAC CTCTAGAACCTACATTTGA AATATTCTGG	60
CAGTGAGGTG TTTCATCCTAA CTCAGTCAGG TAGCTGTGGA CAGCCTTCAC CTGTTAGGAG	120
CTCCTTAGAA ATAAATTCTG AATACCTTTG GTTTTCTTTT ATCCTCCAGA GGAATTTCAGA	180
CTATCTCCGA AGCTGTTCTT TGTTCCACTG ACAATTGCT TAGTTAATGT TCTTTTTAG	240
CCTGTACTAT CTCGAG	256

(2) INFORMATION FOR SEQ ID NO:447:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:447:

GAAGGCAGAA AAATCTATGG AAAGAGAAGG CTACGAGTCC TCGGGCAATG ATGACTACAG	60
GGGTAGTTAC AACACCGTGC TCTCACAGCC TTTATTGAA AAGCAGGACA GAGAAGGTCC	120
AGCCTCCACG GGAAGCAAAC TCACCAATTCA GGAACATCTG TACCCCGCGC CTTCATCACC	180
TGAGAAAGAA CAGCTGCTGG ACCGCAGACC CACTGAATGT ATGATGTCGC GATCAGTAGA	240
TCACCTCGAG	250

(2) INFORMATION FOR SEQ ID NO:448:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 198 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:448:

GAATTGGGCC TTTCATGGCCT AGCTGGGGGG AATAGGTTAT GTGATAAGGA GTCAGTCGGA	60
CAGAGTGGGG TGAAAGATGT TCAGACAGGG AAACACACAT GCAANAGAGG GAAGGTGGGA	120
CACAGCATAT GCNTCCAACA TTGGTAGGG CCGAGGCCAC ATATGGGAGC AGTGAGAGGT	180
TAGGGATCGA CGCTCGAG	198

(2) INFORMATION FOR SEQ ID NO:449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:449:

GAATTTTCT TACCAAGAAA ATTCAATGCTT TACAAATTGT CAGAGGTGCA CATTACTAAT	60
TACAATAGGT CACACTTTT CTATGCGCTT CATTATAATA TTGGCAACTT TATTATGCC	120
CATTACATAC TGTATTATGC TCTTACTTTA TATGCATTG GAG	163

(2) INFORMATION FOR SEQ ID NO:450:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:450:

GAATTGCTGA TATCTTATAA AGGGGACCTT TTTTCTTAC ATTTCTGACG GTTTTTATCA	60
GAATGTATGT ATTAATGCTA TTTGTCTTGT TATATTATT TTATTTCAG CCACTTCTCG	120
AG	122

(2) INFORMATION FOR SEQ ID NO:451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 302 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:451:

GAATTCGGCC TTTCATAGCCT AACTCAAGAT CTCCCATCTA TTAAAGCAGA GGAATAACTT	60
TTGTAGGCTT AATACTGCTT TCTCACTTAG GAAAAGTTGA AATTAAGAAC ACACAGGAAG	120
GGATCATTTTC CTAAGGTTTA TGTCCTCAAC ATCAAATTGA GTTGAAACTT GACTACAGGC	180
CATCTGCTCA TTCAAAGCAT TACAATAAT CTGTCCTATT GATGATCAAAT ATGAGAGCTG	240
AATTGGATGC AGGATTGGAC ATTGCAAGCT GTTCTCCCAA GTGGGATGGA AAGGTGCTCG	300
AG	302

(2) INFORMATION FOR SEQ ID NO:452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 265 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:452:

GAATTCGGCC TTCATGGCCT	ACAAAAAATAT	TTATTTGACT	GAATGATTAA	ATATGCAGTT	60
ATGGTGTAA	ATATATCATG	TGTTATTTGT	TTGTTAAAT	ACAGACATAA	120
TCTTGAACAA	GAAACTACGG	GGATAAATAA	AAGTACCGAG	CCAGATGAGC	180
GAATTCTGAG	AAAAGTATGC	ATCGGAAATC	CACTGAATT	GTAAATGAAA	240
GAACACAGAA	TGGCCCGGAC	TCGAG			265

(2) INFORMATION FOR SEQ ID NO:453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:453:

GAATTCGGCC TTCATGGCCT	ACTTTAATTT	CTCTGAGCAG	TATTTACAG	TTTGATGTA	60
TAAACCTGGC	ACAGATTATG	TTCAGTTTAT	TTCTAAGTTT	AAGTCATGTT	120
ATATTAAGG	ATATTTCTT	TTTTAAAAAA	TCTACAATGT	TTATTTATT	180
TTAACCTCGC	TTCATCACCA	AGGCTGGAGT	AAAGTACGC	GACCTCAGCT	234

(2) INFORMATION FOR SEQ ID NO:454:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:454:

GAATTCGGCC TTCATGGCCT	ACGCACATCC	GCAGTCAGCC	ACCTCGCGCG	CGCCTCCAGG	60
AGCAAGGATG	GAGAGGCTGG	TGATCAGGAT	GCCCTCTGT	CATCTGTCTA	120
GGTTGGGTC	ATGGCAGCAG	TGGTGTGTG	CACAGCACAA	GTGCAAGTGG	180
TGAAAGAGAG	CAGCTGTACA	CACCTGCTTC	CTTAAATGC	TCTTGCAAA	240
AGCCCTCATT	GTGACATGGC	AGAAAAGAA	AGCTGTAAGC	CCAGAAAACA	300
CAGCGAGAAC	CATGGGGTGG	TGATCCAGCC	TGCCTATAAG	GACAAGATAA	360
GCTGGGACTC	CAAAGCTCAA	CCCTCGAG			388

(2) INFORMATION FOR SEQ ID NO:455:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:455:

GAATTCCGCC	TTCATGGCCT	AGCTGATATT	ATTTCTGAGT	TTTTGCTTAT	TTGCTTTCTA	60
CATAGAACATCA	ATAAAATTGA	CAACTAGCAT	TGCCTATATA	TGCAGGTGTC	ATACTATTCA	120
GGGTACTAGT	ATATTGGCCA	CTCAATTATGA	AACTTTCAAGG	TCCTCATATA	TTTCTTTTA	180
TTACAAATGAT	CTACTTATT	CTGATAAATA	TTGGATTAT	AGAGGCTAAA	GGGCTGGGAA	240
AGGAAAACAT	TCGGTACTAC	TTACAACCAT	TTGATACCGAG	TTGTGTCAT	ACAGACCTCA	300
CACAGCAGCA	CCTCGAG					317

(2) INFORMATION FOR SEQ ID NO:456:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:456:

GAATTCCGCC	TTCATGGCCC	ACAAAATGGT	AATACAAATA	AACCACTACT	TACTGCTTT	60
AATGGTAGTT	TGTTTTTTTT	TTTTTGAGAC	AGAGTCTCGC	TGTGCGCCC	AGGCTGGAGT	120
GCAGTGGCGC	GATCTTGGCT	CACTGCAAGC	TCCGCTTTC	GGGTTCACAC	CATTTCCCTG	180
CCTCAGCCTC	CCGAGTAGCT	GGGACTGCGAG	GCGCCCGACT	CCCGGGTTCA	CACCATTCTC	240
CTCCCTCAGA	CTCGAG					256

(2) INFORMATION FOR SEQ ID NO:457:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:457:

GAATTCCGCC	TTCATGGCCT	AGGAGAACATCG	TGAGACCTCT	ATTTCCATAT	CTTTTCTAC	60
TACTGGAATT	TTTATTTTTA	CCATACCCAT	AAATTACTTT	CTATTTAAG	AACCAATAT	120
ATAATTCCTC	AGTTTAGTAA	AAAGTTCTCA	CTTGAAAAGC	TGGTATATGA	ACTTTAGAGG	180
GCAGATTAAT	CAACTGCTAA	ATATTATTA	TCTTTCTTCT	TGGAACCTTC	CAACACAAAA	240
GACAGTTAT	AGAAAACAAA	GTCAGTGTTC	AAAACAGCTG	AATGAACATAT	CTTTGATAT	300
TTTATTTGTT	TTTGTTTTGT	TTTGTTTTGT	TGAGACAGAG	TCTTGCTCTG	TTGTCCAGGC	360
TGGAGAGTAA	TGGCACGATG	ACTGCAACCT	CTGCCTCCCG	GGCTCAAGTG	ATTCTCCTGC	420
CTCAGTCTCT	CGAG					434

(2) INFORMATION FOR SEQ ID NO:458:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 339 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:458:

GAATTCCGCT	TCATGGACGA	GGAGATCGTG	TCCGAGAACG	AAGCCGAGGA	GAGCCACCGG	60
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CAGGACAGCG CCAACCTGCT CATCTTCATC CTGCTGCTCA CCCTCACCAT TCTCACAATC	120
TGGCTCTTCA AGCACCGCCG GGCCCGCTTC CTGCACGAAA CGGGCCTGGC TATGATTTAT	180
GGTCTTTGG TGCCCTTTGT GCTTCGGTAT GGCAATTATG TTCCGAGTGA TGAAATAAT	240
GTGACCCCTGA GCTGTGAAGT GCAGTCAGT CCAACTACCT TACTGGTAAA TGTTAGTGGA	300
AAATTATATG AGTATATGCT GAAAGGAGAG ATACTCGAG	339

(2) INFORMATION FOR SEQ ID NO:459:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 256 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:459:

GAATTCGGCC TTCATGGCCT ACTTATTTTT GTTTCTGTGT GTTTGTTTTA AATGTGTGTG	60
CGCTCATGTG AGTTTGAAGG GAGTTAGATG CAACAGCAGG AGCTGTGCTC AGGGCAGTGG	120
TGTTAATTAT GGAGGGCGTG GGAAGGGCTG GGAAGAGGAG GGGGTTGTAA GACTCCCTT	180
TTCCCTCGCA TGAAACAGA TGCTGGTAC TGAAAGTCTG TCTGCCGTTA TTGGCAAGAG	240
TGACGGAAAG CTCGAG	256

(2) INFORMATION FOR SEQ ID NO:460:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 320 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:460:

GAATTCGGCC TTCATGGCCT AATTTGAAAA TTCATAAGTT TCTACCAATA CTTCCAATTT	60
CAATCCAACA TCTGAGGATC TCCCTAGATT TCCTATTTCC ATGATTATAA CTCTTGTAAC	120
AGATGATAAG AAACATGGAT CTGACTATAC TCAATTATATT CACATATTTT CTCACTGAAAC	180
TAACCTTTT GCTGAATATA ACCAGTCCCC AGCCTTCAA CTGCCCTCTCT CACTTGCCAC	240
CTCTGCATCT TCCCCCACTG TCTTCCTCAG CAATCAGACT GCCTCTTGCC AAGTCATCAC	300
CACAGCACCC CACTCTCGAG	320

(2) INFORMATION FOR SEQ ID NO:461:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 307 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:461:

GAATTCGGCC TTCATGGCCT ACCCTCTACT ATTTTGAAAC CAAATCAACA ACAACCTATT	60
TAGCTGTGCC CCAACCTTTT CCTCCGACCC CCTAACCAAC CCCCTCTAA TACTAACTAC	120
CTGACTCCTA CCCCTCACAA TCATGGCAAG CCAACGCCAC TTATCCAGTG AACCACTATC	180
ACGAAAAAAA CTCTACCTCT CTATACTAA CTCCCTACAA ATCTCCTTAA TTATAACATT	240

CACAGCCACA GAACTAATCA TATTTTATAT CTTCTTCGAA ACCACACTTA TCCCCACCCA	300
TCTCGAG	307

(2) INFORMATION FOR SEQ ID NO:462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:462:

GAATTCCGGCC TTCAATGGCCT AGTACAATT TAAATAATT CTTACAAGTT TATTACCTAA	60
AACTTTGCAA ATAATTGAAG TTAGAAGCTT TGGATTTTGT TTTTAGAGCT TAATCCTTTT	120
CTGTAAGTGG AAATCCTTTT CACTGGTTA TTTTCTTTT GATTTTATT TACTTGACA	180
CCCTAAAGGT TTAGTGTTCG TGTTTTAAA TCTACTGATC GTTTCTTATG AGATTCCCTTA	240
GAGTACCCCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:463:

GAATTCTAGA CCTGCCTCGA GAGGACGCC GAGAGAAATG AGTAGCAACA AAGAGCAGCG	60
GTCAGCAGTG TTCGTGATCC TCTTTGCCCT CATCACCATC CTCATCCTCT ACAGCTCCAA	120
CAGTGCCAT GAGGTCTTCC ATTACGGCTC CCTGCGGGGC CGTAGCCGCC GACCTGTCAA	180
CCTCAAGAAG TGGAGCATCA CTGACGGCTA TGTCCCCATT CTCGGCAACA AGGTAGCGCA	240
GCTGCTTGG GGAGCTCCTC CCTACTGCC AGCAAAACTC GAG	283

(2) INFORMATION FOR SEQ ID NO:464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:464:

GAATTCCGGCC TTCAATGGCCT AAAAAGTGGT TCCTATTTTC CTGGTTGAAC CTTGAGTGAT	60
ACACCCAGTA TTGTACCAAC CAATTAGTAG ACATTATTC TTCTTAGGTC ATATTATTC	120
CAGCTTATAG AGCAAGAAGT TGAAGCTAA AGGGTTAGAT TACTTGCCCA AGGTAATACA	180
GCAAGAATCT TATTTCATCC AACCTAGAGT GAATATTTCG CCCACATCTC GAG	233

(2) INFORMATION FOR SEQ ID NO:465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:465:

GAATTGGCC	TTCATGGCCT	ACTGATGTTG	AAGACGACAC	CACGGCTTTG	ATGGAATATC	60
AGATATTGAA	AATGTCCTCTC	TGCCTGTTCA	TCCTCTGTT	TCTCACACCT	GGTATTTTAT	120
GCATTGTC	TCTCCAATGT	ATATGCACAG	AGAGGCACAG	GCATGTGGAC	TGTTCAAGCA	180
GAACTTGTCT	TACATTACCA	TCTGGACTCG	AAGAGAATAT	TATACATTAA	AACCTGTCCT	240
ATAACCACTT	TACTGATCTG	CATAACCACTG	TAACCCAATA	TACCAATCTG	AGGACCCCTGG	300
ACATTCAAA	CAACAGGCTT	GAAAGCCTGC	CTGCTCATT	ACCTCGGTCT	CTGTTGAAACA	360
TGTCTGCTGC	TAACAACAAAC	ATAAAACITC	TGACAAATC	TGATACTGCT	TATCAGTGGA	420
ATCTTAAATA	TCTGGATGTT	TCTAAGAACAA	TGCTGGAAAA	GGTTGTCCTC	ATTAAAAATA	480
CACTAAGAAG	TCTCGAG					497

(2) INFORMATION FOR SEQ ID NO:466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:466:

GAATTGGCC	TTCATGGCCT	AGCCCCGACT	AGCTTTGCC	TAACTCCCTC	ATCAAAAGAC	60
CCCCCGCCAG	CTTCCCCACAC	CTCATACGCA	GCCACATCTG	CCCTATTCCTC	CATGCTTTCC	120
AGCTTGCCTG	CCCTCCCTCA	TCTCTCCCTG	CCTGTGCAGA	CCTCCACCCCT	TCTTCCCTCC	180
ACCCCTCCAT	CCCCCAATGC	TTGTAGACCT	TCCATTCACT	CCGTCATC	GTGCGTGGTC	240
TCTGATCGTC	CATCACCTGA	CCTCGAG				267

(2) INFORMATION FOR SEQ ID NO:467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:467:

GTTCACATAA	ATATTATACT	AGCATTCTACC	ATCTCACTTC	TAGGAATACT	AGTATATCGC	60
TCACACCTCA	TATCCTCCCT	ACTATGCCTA	GAAGGAATAA	TACTATCGCT	GTTCAATTATA	120
GCTACTCTCA	TAACCCCTCAA	CACCCACTCG	AG			152

(2) INFORMATION FOR SEQ ID NO:468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:468:

CAATATTC	AGCTATACCA	AGCATACAAT	CAACTCCAAG	CTCGGAATTT	TAACTTCATG	60
GCAAACAGAA	AAGCTAGACT	GAGTTATCAG	TGTTGTGAGA	CGAATATTTG	GCCCAACAAG	120
AGTTGTTGGG	GTGGGAGGAG	GGAGAGACAA	AAGGAAAGGA	CTGCCAGCTC	TCAGAGGGTG	180
GAGATGGGGG	ACCTCGAG					198

(2) INFORMATION FOR SEQ ID NO:469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:469:

GAATTCCGCC	TTCATGGCCT	ACTGCTATAT	TCAAGTTCT	CCCACTACTG	TGGTTTCTTT	60
TTTTTTTTT	TTTTTTTTT	TTTGAGACA	GGGTCTTGCT	CTGTCACCCA	GGCTGGGGTG	120
CAGTGGTGC	ATCTCGGCTC	ACTGCAAATT	ACACCTCTG	GATTGAGCA	ATTCTCATGC	180
CTCAGTTCC	TGAGTAGCTG	GGATAACAGG	TATGCACAC	CACCCCTGGC	TAATTTTGT	240
GTTTTAGTA	GAGACAAGTT	CTCACCATGT	TGTCCAAGCC	ACCTCGAG		288

(2) INFORMATION FOR SEQ ID NO:470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:470:

GAATTCCGCC	TTCATGGCCT	AAAAGAAGAA	TACTAATTAG	AATTTGAGTT	CTAGGGTTT	60
TTCCTAGGTT	TTTCATTCTA	GACTTAGCTT	TTATTCAAAC	CTGTTGATCC	TGCATAGGGG	120
TAGCTAGCT	TTAAAAAATA	AAACAATAAA	CATAATGAG	CCTATTGAGT	TCAATCAGAG	180
TAGGGAGCAG	TTTTATTGAA	CAGCACATT	TCAAATTCTT	CAGTTGTGTT	TTGTTTTCA	240
GCTACGTGTC	TCTCTGTGAT	AATGAAAAGA	CAGGTTGCAA	AGCCCCGGAA	CTAAAATCAG	300
TTTATGTGGA	TGCAGTAGGA	CTCGAG				326

(2) INFORMATION FOR SEQ ID NO:471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:471:

GAATTCTGGCC TTCATGGCCT AGTGTAAAGT GTTTTGCAC AGTCCCAGA AATTCGAGT	60
ATTTAATGGT CCTTCCTCCT TATTTATTT TATTACTTGT TTTGTTTTT TTGAGACAGT	120
GTCTTGCTCT GTCGCCCAAGG CTGGAGAGCA GTGATATTAT CGTGAACTCAC GGCAGCCTCG	180
ACCTCCCCAGA CTCAAGGTGAT CCCTTCACCT CAGCCTCCCA GGCAGCTGGG ACCATAGCTA	240
TGAACAAACA CGTCCAGCTA TGTTTTGTAT TTTTGTGAA GACGGAGTCT CACCATGTTG	300
CCCAGGCTGA TCTCCAACTC CTCGAG	326

(2) INFORMATION FOR SEQ ID NO:472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:472:

GGAAAGGTGT TGTCCCTTGT AACATTTGG TTGGCTATAA AGCTGTATAT CGTTTGTGCT	60
TTGGTTTGGC TATGTTCTAT CTTCTTCTCT CTTTACTAAT GATCAAAGTG AAGAGTAGCA	120
GTGATCCTAG ACCTGCAGTG CACAATGGAT TTGGTCTT TAAATTGCT GCAGCAATTG	180
CAATTATTAT TGGGGCATTTC TTCATTCCAG AAGGAACCTT TACAACGTG TGGTTTTATG	240
TAGGCAACCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:473:

GAATTCTGGCC TTCATGGCCT ACAGAAATCT AATTCTGGT GCTATTTGCA ACTACATATA	60
TTTAAATAC AAGGAGATAA ATACCCAGAA CACATTAAGC CTACTGATTT AACAGAACAA	120
TTCAAGACT GCTACACAGA AAGGGAAGGA AGCTGTTAAC CCAGCACAGC ACCACACCTC	180
ACATATTAT GTCTCAGAGA TTAAATGGAA AGAAAGGATC AATCAAACCC TTTATGCTC	240
AGTTTTCAAA AACACAGTCA AGTCTATCAA ATTTCAGAT TTACAG	286

(2) INFORMATION FOR SEQ ID NO:474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:474:

GAATTCTGGCC TTCATGGCCT ACAATTAAAA GGTTCTGTT AATTACGTCT TTCAGTCTGA	60
AATTACTCTG AGAATTACT TAAATTTTT CCATTTAAA ACAGGTATAA AATTAATTGC	120
TAGTTTCCAT AATCACCCAG TATAAAGATA GAAAAGACCT GTAAGACAAC TGTGTGGTTA	180

AATAACATGAT AACACATTTA CGTGCCTTTT ATAGAAATCC ACTTATTATG TACATACTGG	240
CTTGTGTTTTT TTCCCACCTTC TCCAGTACAC TATTTTCAGGC ACAGGCTCAA AATTGAAACC	300
CAAATGGTCT GTTAGGTCTC TTGACTTTTT CAGTTCAAAG CTCTGCTAAT CTGCTAAACC	360
TAGCCCCAAA CCCACTCGAG	380

(2) INFORMATION FOR SEQ ID NO:475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:475:

GAATTCTAGA CCTGCCCGGA GCCCTGACCT AGTCCGGCGT GGAGAGAGGA ATGGAAAGCA	60
GTGTCCTTT TGAGAAGGCA AATTACAGC TGGCTTTGT AATCCTAGCT ATTTTTGTT	120
TGTTTGTAA GTCTTTGATA GTCCCCAGTG TGGTTTGCTC GCCAGTGTAC TCAGCACCAC	180
CAGAGAGCTT GTTAGAAATG CGGCATCCCA ACCCCACCA AGCCCTCCCA AGTCAGATAC	240
TCCCCCTCT CGAG	254

(2) INFORMATION FOR SEQ ID NO:476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:476:

GAATTCGCTG TGGAGCTGGG CGTGCTGTTTC GTCCGGCCCC GGCCCGGAAC CGGGCTGGGT	60
AGAGTGTGCG GGACCCCTCT GCTGGTGTG TGGCTGGCGA CGCGCGGAAG CGCGCTCTAC	120
TTTCACATCG GAGAGACCGA GAAGAACTGC TTTATTGAGG AGATCCCGGA CGAGACCATG	180
GTCATAGGAA ACTACCGGAC GCAGCTGTAT GACAAGCAGC GGGAGGAGTA CCAGCCGGCC	240
ACCCCGGGGC TTGGCATGTT TGTGGAGGTG AAGGACCCAG AGGACAAGGT CATCCTGGCC	300
CGGCAGTATG GTTCCGAGGG CAGGTTCACT TTCANTTCCC ATACCCNTGT GTGAGCACCA	360
GATCTGTTT CANTCCAATT CCACTCGAG	389

(2) INFORMATION FOR SEQ ID NO:477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:477:

GAATTCGGCC TTCACTGGCCT AGAAGGAAAT AAAGGCCCG ATTTCTGGAG TTCTGAGCCT	60
ACTTTTTTG GGTGCATTTT GAAACATACG GATTTTACCG CTAGTATATT CAGTGAGGAA	120
GGAAGGCTTC TGAAGGATTC ATGATCCCCA AACTGGATTA TGTGTTCATG ATAATGGTGT	180
ATTTGGTGGC CTAGCATAGT GAGGTGAGGT AGGTCTTAA AATGGCTCAT TATAAACATC	240

ATTGTTCCCTG AGCTCACTTG CCCTTGCATC TCCGCCAGA GTGCTTTGTA CATACTAGGC	300
CCTCATCAAT GCTTGTAGAT TTTAAATTG GAGGCACACT TGGAAAGACAA TGTTGGCTGG	360
TAAATTAATT ATCAGGGTTA GCAACTTCAT TTCTGCTNAC GCTTAAAAAG TGCTGCGCGA	420
GGAAACTCGA G	431

(2) INFORMATION FOR SEQ ID NO:478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:478:

GCCTCTGNIT TTAATTCAATT GGCAACTGTT ACGATGGAAG ACCTGATTG ACCTTGGTTC	60
CTTGAGTTCT CTGAAGCCCG GGCCATCATG CTTTCCAGAG GCCTTGCCTT TGGCTATGGG	120
CTGTTTGTC TAGGAATGGC CTATATTTCC TCCCGATGG GACCTGTGCT GCAGGCAGCA	180
ATCAGCATCT TTGGCATGGT TGGGGGACCG CTGCTGGAC TCTTCTGCCT TGGAATGTT	240
TTTCCATGTG CTAACCCCTCC TGGTGCTGTT GTGGCCCTGT TGGCTGGCT CGTCATGCC	300
TTCTGGATTG GCATCGGGAG CATCGTGACC AGCATGGCT TCAGCATGCC ACCCTCTCCC	360
TCTAATGGGT CCAGCTTCTC CCTGCCAACC AATCTAACCG TTGCCACTGT GACCACACTT	420
CTCGAG	426

(2) INFORMATION FOR SEQ ID NO:479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:479:

GAATTCCGCC TTCATGGCCT AAATTTCAAG GCAGTTGAA GTATCTGGCA GAAAAAGTAA	60
ATTGAAATCA TTGGGACGTT GATTTTTAAA TTACCTAGAA GCAATCCCAA TGCTTTATGT	120
AATACTAAAA TTTCTCCTCT CTCTTTCTT TATCTCTCTC TCCCTGAAA ATAATCATTT	180
TTTTCCAGT GCCAGTTCAAG ATCTTGGCAA CAGTTGTTT GAAAAAGTAC CTGAACAAAA	240
TACATTTTAT AAAGTAAAGT ATTCAAGAAC TGACAGAACT GGAGAAGAAT ATATTTATGT	300
TACAGAAGTC ATGGACAACC TCGAG	325

(2) INFORMATION FOR SEQ ID NO:480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 406 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:480:

GGCAAGTAAC AGGTTGCAAG AATTGGAGGC AGAGCAACAG CAGATCCAAG AAGAAAGAGA	60
ATTACTGTCC AGACAAAAGG AAGCTATGAA AGCAGAGGCA GCCCAGTTG AACACAAATT	120

ACTACAGGAG ACAGACAAAT TAATGAAGCA AAAACTAGAA GTACAAATGTC AAGCTGAAAA	180
AGTACGTGAT GACCTTCAAA ACAAGTGAA AGCTCTAGAA ATAGATGTGG AAGAACAAAGT	240
CAGTAGGTTT ATAGAGCTGG ACAAGAAAA AAATACTGAA CTAATGGATT TAAGACAGCA	300
AAACCAAGCA TTGGAAAAGC AGTTAGAAAA AATGAGAAAA TTTTTAGATG AGCAAGCCAT	360
TGACAGAGAA CATGAGAGAG ATGTATTCCA ACAGGAAATA CTCGAG	406

(2) INFORMATION FOR SEQ ID NO:481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:481:

GAATTCCGCC AAAGAGGCCT AGTCGGTCCC TCATTGGTAT AAATGTTATG TCTGCATGGG	60
TTTTTCTAC AATTCTTTC TAAGATTATT TCTCCCCAAA GCTCAGCACT TTTGGAATT	120
TTCATTCTCA TCCAAAAATG GAAGCAATT TATGTAATG TCTCTGGAA GCAGTGTGG	180
AATTCTATT TTGGGTAGCA GAAGCAGTAG TTACAAGGGT AGTGGTGTCT TTTGTGGTGG	240
TGGTGGCACC TGCTGCAGTT GTTCATATT GGGGTGCAGG AGTAGGGAGG GTAGGATCAG	300
TTGGAGAATT TACAGGGAAA AATGGAGGTC CAGGTGGATA GGGTCTAGAA TTCAATC	357

(2) INFORMATION FOR SEQ ID NO:482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:482:

GAATTCCGCC AAAGAGGCCT AAGTGACTCC AGAGCCTCCT GCAAGATGCT GTTGATTCTG	60
CTGTCAGTGG CCTTGCTGGC CCTGAGCTCA GCTCAGAACT TAAATGAAGA TGTCAGCCAG	120
GAAGAACATCTC CCTCCCTAAT AGCAGGAAT CCACAAGGGAG CACCCCCACA AGGAGGCAAC	180
AAACCTCAAG GTCCCCCATC TCCTCCAGGA AAGCCACAAG GACCACCCCC ACAAGGAGGC	240
AACCAGCCTC AAGGTCCCCC ACCTCCTCCA GGAAACAC AAGGACCAAC CCCTATTCTC	300
GAG	303

(2) INFORMATION FOR SEQ ID NO:483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:483:

GAATTCCGCC AAAGAGGCCT AAGCAGACAC AATGGTAAGA ATGGTGCCTG TCCTGCTGTC	60
TCTGCTGCTG CTTCTGGGTC CTGCTGTCCC CCAGGAGAAC CAAGATGGTC GTTACTCTCT	120
GACCTATATC TACACTGGGC TGTCCAAGCA TGTGAAGAC GTCCCCCGT TTCAGGCCCT	180

TGGCTCACTC AATGACCTCC AGTTCTTAG ATACAACAGT AAAGACAGGA AGTCTCAGCC	240
CATGGGACTC TGGAGACAGG TGGAGGAAT GGAGGATTGG AAGCAGGACA GCCAACTTCA	300
GAAGGCCAGG GAGGACATCT TTATGGAGAC CCTGAAAGAC ATCGTGGAGT ATTACAACGA	360
CAGTAACGGG TCTCACGTAT TGCAGGAAAG GTTTGGTTGT GAGATCGAGA ATAACAGAAG	420
CAGCGGAGCA TTCTGGAAT ATTACTATGA TGGAAAGGAC AAACCTCGAG	469

(2) INFORMATION FOR SEQ ID NO:484:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 516 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:484:

GAATTGGCC AAAGAGGCCT ACTACTTCTG TAGTCTCATC TTGAGTAAAA GAGAACCCAG	60
CCAATATGA AGTTCCTTGT CTTTGCCTTC ATCTTGCTC TCATGGTTTC CATGATTGGA	120
GCTGATTATCT CTGAAGAGTA TGGGTATGGC CCTTATCAGC CAGTCCAGA ACAACCAGA	180
TACCCACAAAC CATAACCAACC ACAATACCAA CCTGCCTCAA GGTCTCCAC CTCCCTCCAGG	240
AAAGCCACAA GGACCAACCCC CACAAGGAGG CAACAAACCT CAAGGTCCCC CACCTCCAGG	300
AAAGCCACAA CGACCAACCCC CACAAGGAGG CAGCAAGTCC CGAAGTTCTC GATCTCCTCC	360
AGGAAAGCCA CAAGGACCAC CCCACAAGG AGGCAACAAA CCTCAAGGTC CCCCACCTCC	420
AGGAAAGCCA CAAGGACCAC CCCACAAGG AGGCAGGAAG TCCCGAAGTG CCCGATCTCC	480
TCCAGGAAAG CCACAAAGGAC CATCCACAA CTCGAG	516

(2) INFORMATION FOR SEQ ID NO:485:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:485:

GAATTGGCC AAAGAGGCCT ACTTCACTTC AGCTTCACTG ACTTCTTGAC TCTCCTCTTG	60
AGTAAAAGGA CTCAGCCAAC TATGAAGTTT TTGTGCTTTG CTTTAGTCTT GGCTCTCATG	120
ATTTCCATGA TTAGCGCTGA TTCACATGAA AAGAGACATC ATGGGTATAG AAGAAAATTG	180
CATGAAAAGC ATCATTCA CTCGAGAATT CCATTTATG GGGACTGTGG ATCAAATTAT	240
CTATATGACA ATTGATATCC TTAGTAATCA TGGGGCATGA TTATAGAGGT TTGACTGGCA	300
AATTCACTTT TACTCATTTA TTCTCATTCA TCACACCGCA AGTCTAGGCC TCTCGAG	357

(2) INFORMATION FOR SEQ ID NO:486:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 643 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:486: